

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:20:05 ; Search time 20 Seconds

(without alignments)

1351.491 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVGGPSLGTCLV.....NEHLMDHEASFFGAFLVG 281

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

PIR 78:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.8	643	2 G75599	probable drug tran
2	8	2.8	950	2 T09076	hypothetical prote
3	7	2.5	51	2 S63590	insulin - duckbill
4	7	2.5	93	2 F84175	hypothetical prote
5	7	2.5	96	2 P80423	H4 protein - foxop
6	7	2.5	107	2 C90304	hypothetical prote
7	7	2.5	155	2 G72548	hypothetical prote
8	7	2.5	240	2 A39016	T-cell surface gly
9	7	2.5	247	2 D90053	hypothetical prote
10	7	2.5	251	2 T40807	hypothetical prote
11	7	2.5	263	2 T38003	hypothetical ser-t
12	7	2.5	327	2 H82736	ADFGlyceromanno-he
13	7	2.5	329	2 D71887	hypothetical prote
14	7	2.5	354	2 G71465	hypothetical prote
15	7	2.5	354	2 A81728	conserved hypotet
16	7	2.5	401	2 C82660	conserved hypotet
17	7	2.5	404	2 G90210	hypothetical prote
18	7	2.5	420	2 S53916	SUN4 protein precu
19	7	2.5	424	2 H84806	hypothetical prote
20	7	2.5	427	2 G71272	iron-sulfur cofact
21	7	2.5	428	2 E84192	zinc metalloprotei
22	7	2.5	429	2 B72109	GMP synthase CP059
23	7	2.5	429	2 C86512	GMP synthase limpo
24	7	2.5	442	2 AF2539	manganese transpor
25	7	2.5	475	2 T39359	probable udp-n-ace
26	7	2.5	511	2 T19496	hypothetical prote
27	7	2.5	554	2 A47503	epoxide hydrolase
28	7	2.5	565	2 C82280	sensor kinase cita
29	7	2.5	710	2 T22360	hypothetical prote

30	7	2.5	801	2 AE3032	conserved hypotet
31	7	2.5	801	2 G98253	hypothetical prote
32	7	2.5	809	2 T20430	hypothetical prote
33	7	2.5	913	2 D90183	ATP-dependent heli
34	7	2.5	926	2 T15683	hypothetical prote
35	7	2.5	979	2 JH0109	glycoprotein 14 pr
36	7	2.5	982	2 E88465	protein B0244.6 [1
37	7	2.5	1014	2 T36031	excinuclease ABC c
38	7	2.5	1377	2 T19214	UDP-glucose-glycop
39	7	2.5	1414	2 T33236	hypothetical prote
40	7	2.5	1447	2 E64477	replication factor
41	7	2.5	1891	2 T43262	calcium channel al
42	7	2.5	1975	2 B81192	hemagglutinin/hemo
43	7	2.5	1995	2 G81044	hypothetical prote
44	7	2.5	2015	2 B81989	genome polyprotein
45	7	2.5	3434	1 GNWVWV	ethylene responsiv
46	6	2.1	47	2 T04365	H+-transporting tw
47	6	2.1	48	2 S78202	hypothetical prote
48	6	2.1	55	2 AF2105	hypothetical prote
49	6	2.1	56	2 C60157	hypothetical prote
50	6	2.1	62	2 C97621	probable bacteriof
51	6	2.1	64	2 AG0025	hypothetical prote
52	6	2.1	65	2 AC0774	hypothetical prote
53	6	2.1	85	2 C91249	protein YDR363W-a
54	6	2.1	89	2 S78744	conserved hypotet
55	6	2.1	96	2 B82311	transposase tnp [i
56	6	2.1	96	2 AE3205	hypothetical prote
57	6	2.1	98	2 G91248	probable cytochrom
58	6	2.1	102	2 C95337	conserved hypotet
59	6	2.1	104	2 B69832	hypothetical prote
60	6	2.1	105	2 B86818	hypothetical prote
61	6	2.1	107	2 S09964	Ig kappa chain V-J
62	6	2.1	107	2 A44887	glucose transporte
63	6	2.1	109	2 F84012	hypothetical prote
64	6	2.1	112	2 AC2887	conserved hypotet
65	6	2.1	112	2 H97662	hypothetical prote
66	6	2.1	115	2 B25924	Ig kappa chain pre
67	6	2.1	116	2 C83166	probable chaperone
68	6	2.1	117	2 F97174	hypothetical prote
69	6	2.1	119	2 JQ2032	lambda 208 protein
70	6	2.1	122	2 D89803	conserved hypotet
71	6	2.1	128	2 AH0043	probable lipoprote
72	6	2.1	130	2 D64559	hypothetical prote
73	6	2.1	132	2 F66829	ribose ABC transpo
74	6	2.1	132	2 F70650	hypothetical prote
75	6	2.1	134	2 AC0855	probable regulator
76	6	2.1	135	2 B91078	transcription regu
77	6	2.1	135	2 T44999	hypothetical prote
78	6	2.1	137	2 S74888	conserved hypotet
79	6	2.1	137	2 D86944	hypothetical prote
80	6	2.1	137	2 T30095	hypothetical prote
81	6	2.1	137	2 F89954	conserved hypotet
82	6	2.1	143	1 WMBEGH	transcription regu
83	6	2.1	143	2 T43976	transactivator lim
84	6	2.1	143	2 B71372	conserved hypotet
85	6	2.1	145	2 AC0053	DNA-directed DNA p
86	6	2.1	146	2 C85923	probable regulator
87	6	2.1	149	2 H70581	hypothetical prote
88	6	2.1	151	2 A75297	hypothetical prote
89	6	2.1	152	2 B64485	hypothetical prote
90	6	2.1	152	2 T43088	traJ protein homol
91	6	2.1	154	2 F90546	deoxycytidylate de
92	6	2.1	157	2 A84402	hypothetical prote
93	6	2.1	161	2 H87183	integral membrane
94	6	2.1	162	2 T50253	Vacuolar ATP synth
95	6	2.1	165	2 S62563	adaptin complex sm
96	6	2.1	166	2 A75426	hypothetical prote
97	6	2.1	167	2 G95335	hypothetical prote
98	6	2.1	169	2 D72765	hypothetical prote
99	6	2.1	169	2 T31484	hypothetical prote
100	6	2.1	170	2 T48974	hypothetical prote

ALIGNMENTS

RESULT 1

G75599
 Probable drug transport protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 R:Accession: G75599
 A:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Shen, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: G75599
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-643 <WHI>
 A:Cross-references: GB:AE001862; GB:AE001825; NID:G6460468; PIDN:AAF12254.1; PID:G646054
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRA0061
 A:Map position: 2

Query Match 2.8%; Score 8; DB 2; Length 643;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VLIVITV 24

|||||

Db 231 VLIVITV 238

RESULT 2

T09076
 Hypothetical protein Cg1 (strain HB3) - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
 C:Accession: T09076
 R:Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellem, T.E.
 Cell 91, 593-603, 1997
 A:Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant
 A:Reference number: Z16556; MUID:98054002; PMID:9393853
 A:Accession: T09076
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-950 <SUX>
 A:Cross-references: EMBL:AF030690; NID:G2642510; PIDN:AAC47851.1; PID:G2642511
 C:Genetics:
 A:Gene: cgl

Query Match 2.8%; Score 8; DB 2; Length 950;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140

|||||

Db 361 SNTLSSPN 368

RESULT 3

S63590
 Insulin - duckbill platypus
 C:Species: Ornithorhynchus anatinus (duckbill platypus)
 C:Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: S63590
 R:Nourse, A.; Treacy, G.B.; Shaw, D.C.; Jeffrey, P.D.
 Biol. Chem. Hoppe-Seyler 377, 147-153, 1996
 A:Title: Platypus insulin: indications from the amino acid sequence of significant differ
 A:Reference number: S63590; MUID:97021710; PMID:8868070
 A:Accession: S63590
 A:Molecule type: protein

A:Residues: 1-30 <NOU2>
 A:Accession: S63590
 A:Molecule type: protein
 A:Residues: 31-51 <NOU1>
 C:Superfamily: insulin
 C:Keywords: hormone; pancreas
 F:1-30/31-51/Product: insulin #status experimental <MAT>
 F:1-30/Domain: insulin chain B #status experimental <BCH>
 F:31-51/Domain: insulin chain A #status experimental <ACH>
 F:7-37,19-50,36-41/Disulfide bonds: #status predicted

Query Match 2.5%; Score 7; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 EKGFIYI 184

|||||

Db 21 EKGFIYI 27

RESULT 4

F84175
 Hypothetical protein Vng0151c [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84175
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.
 Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl.
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: AB4160; MUID:20504483; PMID:11016950
 A:Accession: F84175
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-93 <STO>
 A:Cross-references: GB:AE004437; NID:gl0579798; PIDN:AAG18770.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG0151C

Query Match 2.5%; Score 7; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 FVSVTNE 263

|||||

Db 13 FVSVTNE 19

RESULT 5

PS0423
 H4 protein - Toxoplasma gondii (fragment)
 N:Alternate names: diagnostic antigen H4
 C:Species: Toxoplasma gondii
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Sep-1997
 C:Accession: PS0423
 R:Johnson, A.M.; Illana, S.
 Gene 99, 127-132, 1991
 A:Title: Cloning of Toxoplasma gondii gene fragments encoding diagnostic antigens.
 A:Reference number: PS0423; MUID:91216437; PMID:2022319
 A:Accession: PS0423
 A:Molecule type: mRNA
 A:Residues: 1-96 <JOH>
 A:Cross-references: GB:M57302; NID:gl161914; PID:gl161915
 C:Genetics:
 A:Gene: H4

Query Match 2.5%; Score 7; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEEIKE 198

Db 2 FOEBIKE 8
|||||

RESULT 6

C90304
hypothetical protein SS01462 [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C/Accession: C90304
R/Shu, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jung, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: C90304
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-107 <KUR>
A/Cross-references: GB:AE006641; NID:gl3814690; PIDN:AAK41690.1; GSPDB:GN00155
C/Genetics:
A/Gene: SS01462

Query Match 2.5%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 FFGAFLV 280
|||||
Db 46 FFGAFLV 52

RESULT 7

G72548
hypothetical protein APE1675 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C/Accession: G72548
R/Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah-
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: G72548
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-155 <KAW>
A/Cross-references: DDBJ:AP000062; NID:gs105244; PIDN:BAAS0676.1; PID:d1044462; PID:gs10
A/Experimental source: strain K1
C/Genetics:
A/Gene: APE1675

Query Match 2.5%; Score 7; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TLSSPNS 141
|||||
Db 88 TLSSPNS 94

RESULT 8

A39016
T-cell surface glycoprotein CD7 precursor - human
N/Alternate names: T-cell leukemia antigen
C/Species: Homo sapiens (man)
C/Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
C/Accession: A39016; S03520
R/Schanberg, L.E.; Fleener, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 603-607, 1991
A/Title: Isolation and characterization of the genomic human CD7 gene: structural simila
A/Reference number: A39016; MUID:91110576; PMID:1703303

A/Accession: A39016
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-240 <SCH>
A/Cross-references: GB:M37271; NID:gl80163; PIDN:AAA51953.1; PID:gl80164
R/Aruffo, A.; Seed, B.
EMBO J. 6, 3313-3316, 1987
A/Title: Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell ex
A/Reference number: S03520; MUID:88111517; PMID:3501369

A/Accession: S03520
A/Molecule type: mRNA
A/Residues: 1-240 <ARU>
A/Cross-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757
C/Genetics:
A/Gene: GDB:CD7
A/Cross-references: GDB:119770; OMIM:186820
A/Map position: 17q25.2-17q25.3
A/Introns: 28/1
C/Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-240/Product: T-cell surface glycoprotein CD7 #status predicted <MAT>
F:145-180/Region: 9-residue repeats [X-P-P-X-A-S-A-L-P]

Query Match 2.5%; Score 7; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 NTLSSPN 140
|||||
Db 231 NTLSSPN 237

RESULT 9

D90053
hypothetical protein sarH2 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: D90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Og
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146

A/Accession: D90053
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-247 <KUR>
A/Cross-references: GB:BA000018; PID:gl3702449; PIDN:BA843590.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: sarH2

Query Match 2.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
|||||
Db 91 RIFVSVT 97

RESULT 10

T40807
hypothetical protein SPBP87.13 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C/Accession: T40807
R/Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A/Reference number: Z21949
A/Accession: T40807
A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-251 <BEC>

A:Cross-references: ENBL:AL032684; PIDN:CAA21798.1; GSPDB:GN00067; SPDB:SPBP8B7.13

A:Experimental source: strain 972h-; clone pl p857

C:Genetics:

A:Gene: SPDB:SPBP8B7.13

A:Map position: 2

A:Introns: 54/1

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBP8B7.13

Query Match 2.5%; Score 7; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DNDEES 72

DB 73 DNDEES 79

RESULT 11

T38003 hypothetical ser-thr rich protein - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Nov-2000

C:Accession: T38003

R:Oliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the ENBL Data Library, June 1997

A:Reference number: Z21760

A:Accession: T38003

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-263 <OLI>

A:Cross-references: ENBL:Z97209; PIDN:CAB10128.1; GSPDB:GN00066; SPDB:SPAC19G12.16c

A:Experimental source: strain 972h-; cosmid c19G12

C:Genetics: SPAC23A1.01c; SPDB:SPAC19G12.16c

A:Map position: 1

C:Superfamily: Yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 263;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 EETISTV 103

DB 177 EETISTV 183

RESULT 12

H82736

hypothetical protein XF0992 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: H82736

C:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82736

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 <SIM>

A:Cross-references: GB:AE003937; GB:AE003849; NID:g9105920; PIDN:AAF83802.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carzer, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.J.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; ;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0992

Query Match 2.5%; Score 7; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117

DB 164 SPLVRER 170

RESULT 13

D71887

ADPglyceromanno-heptose 6-epimerase (EC 5.1.1.3.20) gmhD homolog [similarity] - Helicobac

C:Species: Helicobacter pylori

A:Variety: strain J99

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000

C:Accession: D71887

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat.

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71887

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-329 <ARN>

A:Cross-references: GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD06369.1; PID:g415535

A:Experimental source: strain J99

C:Genetics:

A:Gene: gmhD

C:Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology

C:Keywords: isomerase

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 329;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTLSS 138

DB 46 RSNTLSS 52

RESULT 14

G71465

hypothetical protein CT839 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: G71465

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell

Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A:Reference number: A71570; MUID:9900809; PMID:9784136

A:Accession: G71465

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-354 <ARN>

A:Cross-references: GB:AE001356; GB:AE001273; NID:g3329299; PIDN:AAC68436.1; PID:g33293

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT839

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 354;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
|||||
Db 150 KENDRIF 156

RESULT 15

A81728
Conserved hypothetical protein TC0227 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: A81728
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10664935
A:Accession: A81728
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <TGT>
A:Cross-references: GB:AE002289; GB:AE002160; NID:g7190254; PIDN:AAF39099.1; PID:g7190264
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0227

Query Match 2.5%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
|||||
Db 150 KENDRIF 156

RESULT 16

C82660
Conserved hypothetical protein XF1611 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: C82660
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82660
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <SIM>
A:Cross-references: GB:AE003988; GB:AE003849; NID:g9106653; PIDN:AAF84420.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328
A:Status: annotation
C:Genetics:
A:Gene: XF1611
C:Superfamily: Escherichia coli hypothetical 48K protein (glnA-fdhE region)

Query Match 2.5%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 DAEGLY 240
|||||
Db 157 DAEGLY 163

RESULT 17

G90210
hypothetical protein purF-2 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: G90210
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chai Jung, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90210
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813800; PIDN:AAK40942.1; GSPDB:GN00155
C:Genetics:
A:Gene: purF-2

Query Match 2.5%; Score 7; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YSKSGIA 55
|||||
Db 35 YSKSGIA 41

RESULT 18

S53916
SUN4 protein precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein N2411; protein YNL066w; protein YNL1612
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C:Accession: S53916; S58712; S62994; S62998; S63945
R:Poehmann, R.; Philippsen, P.
submitted to the EMBL Data Library, April 1995
A:Reference number: S53896
A:Accession: S53916
A:Molecule type: DNA
A:Residues: 1-420 <POE>
A:Cross-references: EMBL:X86470; NID:g791101; PID:g791122
R:Bergez, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
A:Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XI
A:Reference number: S58711; MUID:96021608; PMID:8533472
A:Accession: S58712
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-420 <BER>
A:Cross-references: EMBL:U12141; NID:gl314216; PIDN:AAA99645.1; PID:g994821
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R:Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S62975
A:Accession: S62994
A:Molecule type: DNA
A:Residues: 1-420 <BEF>
A:Cross-references: EMBL:Z71342; NID:gl301944; PID:gl301945; MIPS:YNL066w
R:Poehmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S62997
A:Accession: S62998
A:Molecule type: DNA
A:Residues: 1-420 <FOV>
A:Cross-references: EMBL:Z71342; NID:gl301944; PID:gl301945; MIPS:YNL066w

A;Experimental source: strain S288C
R;Pohlmann, R.; Philippsen, P.
Yeast 12, 391-402, 1996

A;Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12
A;Reference number: S63925; MUID:96267764; PMID:8701611

A;Accession: S63945
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-420 <POF>

A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60196.1; PID:g791122

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

C;Genetics:

A;Gene: SGD:SUN4

A;Cross-references: SGD:S0005010; MIPS:YNL066W

A;Map position: 14L

A;Genome: nuclear

C;Superfamily: *Saccharomyces* NCA3 protein

C;Keywords: mitochondrion

F;1-46/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;46-420/Product: SUN4 protein #status predicted <MAT>

Query Match 2.5%; Score 7; DB 2; Length 420;

Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VAVTVVY 37

Db 47 VAVTVVY 53

RESULT 19

H84806

hypothetical protein At2g38590 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C;Accession: H84806

R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84806

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-424 <STO>

A;Cross-references: GB:AE002093; NID:g3786013; PIDN:AAC67359.1; GSPDB:GNO0139

C;Genetics:

A;Gene: At2g38590

A;Map position: 2

C;Superfamily: Arabidopsis thaliana hypothetical protein TIF15.9

Query Match 2.5%; Score 7; DB 2; Length 424;

Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 CFLKEDD 62

Db 122 CFLKEDD 128

RESULT 20

I71272

iron-sulfur cofactor synthesis protein nifS2 TP0863 [similarity] - syphilis spirochete
N;Contains: L-cysteine sulfotransferase (EC 2.8.1.-)

C;Species: *Treponema pallidum* subsp. pallidum (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 20-Jun-2000

C;Accession: G71272

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin-

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Childambaram, M.; Utterback, T.; McD-

vey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A;Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.

A;Reference number: A71250; MUID:98332770; PMID:9665876

A;Accession: G71272

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-427 <COL>

A;Cross-references: GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC65826.1; PID:g33231-

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0863

C;Superfamily: nitrogen fixation protein nifs

C;Keywords: phosphoprotein; pyridoxal phosphate; sulfotransferase

F;23/Binding site: Pyridoxal phosphate (lys) (covalent) #status predicted

F;374/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 2.5%; Score 7; DB 2; Length 427;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGTRGRS 133

Db 166 TGTRGRS 172

RESULT 21

B84192

zinc metalloproteinase homolog [imported] - *Halobacterium* sp. NRC-1

C;Species: *Halobacterium* sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: B84192

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Barquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.

Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl-

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.

A;Title: Genome sequence of *Halobacterium* species NRC-1.

A;Reference number: B84160; MUID:20504483; PMID:11016950

A;Accession: B84192

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-428 <STO>

A;Cross-references: GB:AE004437; NID:g10579955; PIDN:AAG18905.1; GSPDB:GNO0138

C;Genetics:

A;Gene: caax

Query Match 2.5%; Score 7; DB 2; Length 428;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 SSRSGHS 162

Db 237 SSRSGHS 243

RESULT 22

B72109

GMP synthase CP0599 [imported] - *Chlamydia pneumoniae* (strains CWL029 and AR39)

C;Species: *Chlamydia pneumoniae*, *Chlamydia pneumoniae*

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C;Accession: B72109; B81558

R;Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: B72109

A;Molecule type: DNA

A;Residues: 1-429 <ARN>

A;Cross-references: GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD18324.1; PID:g43764-

A;Experimental source: strain CWL029

R;Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; McClarty, J.; Salizberg

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81558
A;Molecule type: DNA
A;Residues: 1-429 <PEA>
A;Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38415.1; PID:g718951
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: guaA; CP0599
C;Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology
P;11-194/Domain: trpG homology <TRG>

Query Match 2.5%; Score 7; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 ESSRSQH 161
|||||
Db 248 ESSRSQH 254

RESULT 23
C86512
GMP synthase [imported] - Chlamydomonas pneumoniae (strain J138)
C;Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001
C;Accession: C86512
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: C86512
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-429 <STO>
A;Cross-references: GB:BA000008; NID:g8978544; PIDN:BAA98381.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: guaA
C;Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

Query Match 2.5%; Score 7; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 ESSRSQH 161
|||||
Db 248 ESSRSQH 254

RESULT 24
AF2539
manganese transport protein all7601 [imported] - Nostoc sp. (strain PCC 7120) plasmid pC
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF2539
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2539
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-442 <KUR>
A;Cross-references: GB:AF003602; PIDN:BAF77244.1; PID:g17134686; GSPDB:GN00181
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all7601
C;Superfamily: natural resistance-associated macrophage protein 1

Query Match 2.5%; Score 7; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 LLOSLCV 31
|||||
Db 76 LLOSLCV 82

RESULT 25
T39359
probable udp-n-acetylglucosamine pyrophosphorylase - fission yeast (Schizosaccharomyces
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39359
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21848
A;Accession: T39359
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-475 <WOO>
A;Cross-references: EMBL:AL035675; PIDN:CAB38688.1; GSPDB:GN00067; SPDB:SPBC1289.08
A;Experimental source: strain 972h-; cosmid C1289
C;Genetics:
A;Gene: SPDB:SPBC1289.08
A;Map position: 2

Query Match 2.5%; Score 7; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSEETIS 101
|||||
Db 168 TSEETIS 174

RESULT 26
T19496
hypothetical protein C27A7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C;Accession: T19496
R;Harris, B.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19132
A;Accession: T19496
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-511 <WIL>
A;Cross-references: EMBL:Z81041; PIDN:CAB02786.1; GSPDB:GN00023; CESP:C27A7.2
A;Experimental source: clone C27A7
C;Genetics:
A;Gene: CESP:C27A7.2
A;Map position: 5
A;Introns: 44/3; 87/2; 130/2; 164/3; 203/2; 273/3; 325/1; 369/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F07G11.3

Query Match 2.5%; Score 7; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 YKSGIA 55
|||||
Db 120 YKSGIA 126

RESULT 27
A47503
epoxide hydrolase (EC 3.3.2.3), cytosolic - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A47503; S17104; S19319
R;Knehr, M.; Thomas, H.; Arand, M.; Gebel, T.; Zeller, H.D.; Oesch, F.
J. Biol. Chem. 268, 17623-17627, 1993

A>Title: Isolation and characterization of a cDNA encoding rat liver cytosolic epoxide hydrolase
 A:Reference number: A47503; MUID:93352557; PMID:8349641
 A:Accession: A47503
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-554 <KNE>
 A:CROSS-references: GB:X65083; NID:9402631; PIDN:CAA46211.1; PID:9402632
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBIN:136329, NCBIP:136330)
 A:Residues: 1-710 <WIL>
 A:Cross-references: EMBL:Z99171; PIDN:CAB16314.1; GSPDB:GN00019; CESP:F47G4.2
 A:Experimental source: clone F47G4
 A:Genetics:
 A:Gene: CESP:F47G4.2
 A:Map position: 1
 A:Introns: 20/1; 131/3; 220/2; 273/1; 380/2; 577/2

Query Match 2.5%; Score 7; DB 2; Length 710;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ILRTSEE 98
 DB 647 ILRTSEE 653

RESULT 30

AE3032
 conserved hypothetical protein Atu3866 [imported] - Agrobacterium tumefaciens (strain C)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AE3032
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.; Karp, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AE3032

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-801 <KUR>

A:CROSS-references: GB:AE008689; PIDN:AAL44675.1; PID:gl7742302; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu3866

A:Map position: linear chromosome

Query Match 2.5%; Score 7; DB 2; Length 801;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
 DB 216 ASFFGAF 222

RESULT 31

G98253
 hypothetical protein AGR L1958 [imported] - Agrobacterium tumefaciens (strain C58, Cer)
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C:Accession: G98253
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58
 A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: G98253

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-801 <KUR>

A:CROSS-references: GB:AE007870; PIDN:AAK89553.1; PID:gl5159435; GSPDB:GN00170

Query Match 2.5%; Score 7; DB 2; Length 554;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151
 DB 477 KALGRKI 483

RESULT 28

C82280
 sensor kinase citA VC0791 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: C82280
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Charadon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J.; R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: C82280

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-565 <HEI>

A:CROSS-references: GB:AE004164; GB:AE003852; NID:g9655232; PIDN:AAF93956.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0791

A:Map position: 1

C:Superfamily: two-component sensor histidine kinase; sensor histidine kinase homology

Query Match 2.5%; Score 7; DB 2; Length 565;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVLL 26
 DB 185 VIFTVLL 191

RESULT 29

T22360
 hypothetical protein F47G4.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Genetics:
A;Gene: AGR_L1958
A;Map position: linear chromosome

Query Match 2.5%; Score 7; DB 2; Length 801;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 ASFFGAF 278
|||||
Db 216 ASFFGAF 222

RESULT 32

T20430

hypothetical protein E03A3.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T20430

R;Gardner, A.

submitted to the EMBL Data Library, October 1994

A;Reference number: Z19274

A;Accession: T20430

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-809 <WIL>

A;Cross-references: EMBL:Z38112; PIDN:CAA86232.1; GSPDB:GN00021; CESP:E03A3.2

A;Experimental source: clone E03A3

C;Genetics:

A;Gene: CESP:E03A3.2

A;Map position: 3

A;Introns: 49/3; 144/1; 319/2; 376/3; 484/2; 540/3; 573/2; 612/3; 720/3; 776/3

Query Match

2.5%; Score 7; DB 2; Length 809;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 EYGLYSI 242

|||||

Db 756 EYGLYSI 762

RESULT 33

D90183

ATP-dependent helicase [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C;Accession: D90183

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Feng, X.; Thi-Ngoc, H.P.; Redder, H.

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: D90183

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-913 <KUR>

A;Cross-references: GB:AE006641; NID:g13813545; PIDN:AAK40723.1; GSPDB:GN00155

C;Genetics:

A;Gene: SS00394

Query Match

2.5%; Score 7; DB 2; Length 913;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 ENDRIFV 258

|||||

Db 517 ENDRIFV 523

RESULT 34

T15683

hypothetical protein C28C12.10 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T15683

R;Miller, N.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid C28C12.

A;Reference number: Z18387

A;Accession: T15683

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-926 <MIL>

A;Cross-references: EMBL:U40797; NID:g1065916; PID:g1065927; PIDN:AAB37553.1; GSPDB:GN

A;Experimental source: strain Bristol N2; clone C28C12

C;Genetics:

A;Gene: CESP:C28C12.10

A;Map position: 4

A;Introns: 18/3; 98/2; 173/2; 206/3; 298/3; 405/3; 488/3; 727/3; 761/1; 828/2

Query Match

2.5%; Score 7; DB 2; Length 926;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 DEESMNS 75

|||||

Db 122 DEESMNS 128

RESULT 35

JH0109

glycoprotein 14 precursor - equine herpesvirus 1

C;Species: equine herpesvirus 1

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 26-Aug-1999

C;Accession: JH0109

R;Guo, P.

Gene 87, 249-255, 1990

A;Title: Characterization of the gene and an antigenic determinant of equine herpesvir

A;Reference number: JH0109; MUID:90236317; PMID:1692002

A;Accession: JH0109

A;Molecule type: DNA

A;Residues: 1-979 <GUO>

A;Cross-references: GB:M34861; NID:g330900; PIDN:AAA46086.1; PID:g330901

A;Note: Glycoprotein 14 is homologous to corresponding glycoprotein of pseudorabies, b

C;Genetics:

A;Superfamily: herpesvirus glycoprotein B

C;Keywords: glycoprotein; transmembrane protein

F;1-86/Domain: signal sequence #status predicted <SIG>

F;87-979/Product: glycoprotein 14 #status predicted <MAT>

F;831-871/Region: hydrophobic

F;165,275,380,423,497,514,560,727,749,951,970/Binding site: carbohydrate (Asn) (covalen

Query Match

2.5%; Score 7; DB 2; Length 979;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 SGIACFL 58

|||||

Db 839 SGIACFL 845

RESULT 36

E88465

protein B0244.6 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C;Accession: E88465

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_e

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; ai

A:Accession: E88465
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-982 <STO>
 A:Cross-references: GB:chr_III; PIDN:AAA68379.1; PID:G861359; GSPDB:GN00021; CESP:B0244.
 C:Genetics:
 A:Gene: B0244.6
 A:Map position: 3

Query Match 2.5%; Score 7; DB 2; Length 982;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTLSS 138
 |||||
 DB 461 RSNTLSS 467

RESULT 37

T36031
 excinuclease ABC chain A SCC54.18c [similarity] - Streptomyces coelicolor
 N:Contains: excision endonuclease ABC (EC 3.1.1.-) chain A
 C:Species: streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001
 C:Accession: T36031
 R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: Z21581
 A:Accession: T36031
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1014 <SE>
 A:Cross-references: EMBL:AL035591; PIDN:CAB38148.1; GSPDB:GN00070; SCODEB:SCC54.18c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: uvrA; SCODEB:SCC54.18c
 C:Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
 C:Keywords: ATP; DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop
 F:32-39/Region: nucleotide-binding motif A (P-loop)
 F:645-652/Region: nucleotide-binding motif A (P-loop)

Query Match 2.5%; Score 7; DB 2; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117
 |||||
 DB 153 SPLVRER 159

RESULT 38

T19214
 UDP-glucose-glycoprotein glucosyltransferase (EC 2.4.1.-) precursor F26H9.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T19214; T21444
 R:Barlow, K.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19091
 A:Accession: T19214
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1377 <WIL>
 A:Cross-references: EMBL:Z81467; PIDN:CAB03874.1; GSPDB:GN00019; CESP:F26H9.8
 A:Experimental source: clone C1208
 R:Baynes, C.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19422

A:Accession: T21444
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1377 <W12>
 A:Cross-references: EMBL:Z81516; PIDN:CAB04207.1; GSPDB:GN00019; CESP:F26H9.8

A:Experimental source: clone F26H9
 C:Genetics:
 A:Gene: CESP:F26H9.8
 A:Map position: 1

A:Introns: 40/2; 70/1; 152/2; 318/2; 429/3; 494/2; 538/3; 564/3; 625/3; 654/3; 782/3; 8;
 C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

Query Match 2.5%; Score 7; DB 2; Length 1377;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHLRNG 172
 |||||
 DB 1014 NLHLRNG 1020

RESULT 39

T33236
 hypothetical protein T10H9.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33236
 R:Greco, T.; Bradshaw, H.; O'Brien, D.
 submitted to the EMBL Data Library, May 1998
 A:Description: The sequence of C. elegans cosmid T10H9.
 A:Reference number: Z21306
 A:Accession: T33236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1414 <GRE>
 A:Cross-references: EMBL:AF067949; PIDN:AAC19236.1; GSPDB:GN00023; CESP:T10H9.2
 A:Experimental source: strain Bristol N2; clone T10H9
 C:Genetics:
 A:Gene: CESP:T10H9.2
 A:Map position: 5
 A:Introns: 56/3; 76/1; 101/1; 161/1; 196/1; 226/3; 269/2; 318/1; 364/1; 475/3; 520/2; 5;

Query Match 2.5%; Score 7; DB 2; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 RGPORVA 123
 |||||
 DB 1110 RGPORVA 1116

RESULT 40

E64477
 replication factor C homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: E64477
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Xson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: E64477
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1847 <BUL>
 A:Cross-references: GB:U67583; GB:L77117; NID:G2826409; PIDN:AAB99433.1; PID:G1592072;
 C:Genetics:
 A:Map position: REV1393176-1387633
 A:Start codon: TTG

Query Match 2.5%; Score 7; DB 2; Length 1847;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 IFELKEN 253

Db 877 IFELKEN 883
|||||

RESULT 41

T43262
calcium channel alpha-1 chain, L-type - Stylophora pistillata
C/Species: Stylophora pistillata
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C/Accession: T43262
R/Zoccola, D.; Tamburte, E.; Senegas-Balas, F.; Michiels, J.F.; Falla, J.P.; Jaubert, J.
Gene 227, 157-167, 1999
A/Title: Cloning of a calcium channel alpha subunit from the reef-building coral, *Stylophora pistillata*
A/Reference number: 222375; MUID:99148007; PMID:10023047
A/Accession: T43262
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1891 <ZOC>
A/Cross-references: EMBL:U64465; NID:g4204977; PID:g4204978; PIDN:AAD11470.1
C/Genetics:
A/Gene: CACHL
C/Supfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 2.5%; Score 7; DB 2; Length 1891;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 FLKEDDS 63
|||||
Db 1621 FLKEDDS 1627

RESULT 42

B81192
hemagglutinin/hemolysin-related protein NMB0497 [imported] - *Neisseria meningitidis* (strain Z2491)
C/Species: *Neisseria meningitidis*
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C/Accession: B81192
R/Tettein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter
A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: B81192
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1975 <TET>
A/Cross-references: GB:AE002406; GB:AE002098; NID:g7225720; PIDN:AAF40929.1; PID:g7225720
A/Experimental source: serogroup B, strain MC58
C/Genetics:
A/Gene: NMB0497

Query Match 2.5%; Score 7; DB 2; Length 1975;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
|||||
Db 557 AAHITGT 563

RESULT 43

G81044
hemagglutinin/hemolysin-related protein NMB1779 [imported] - *Neisseria meningitidis* (strain Z2491)
C/Species: *Neisseria meningitidis*
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C/Accession: G81044
R/Tettein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: G81044
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1995 <TET>
A/Cross-references: GB:AE002527; GB:AE002098; NID:g7227023; PIDN:AAF42119.1; PID:g7227023
A/Experimental source: serogroup B, strain MC58
C/Genetics:
A/Gene: NMB1779

Query Match 2.5%; Score 7; DB 2; Length 1995;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
|||||
Db 560 AAHITGT 566

RESULT 44

B81989
hypothetical protein NMA0688 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup B)
C/Species: *Neisseria meningitidis*
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C/Accession: B81989
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
Holroyd, S.; Jageis, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea
Nature 404, 502-506, 2000
A/Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: B81989
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2015 <PAR>
A/Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83974.1; PID:g7379120
A/Experimental source: serogroup A, strain Z2491
C/Genetics:
A/Gene: NMA0688

Query Match 2.5%; Score 7; DB 2; Length 2015;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
|||||
Db 560 AAHITGT 566

RESULT 45

GNVWVW
genome polyprotein - Murray Valley encephalitis virus (strain Australia)
N/Contains: capsid protein; envelope protein; membrane protein; nonstructural protein 1
a; nonstructural protein NS4b; nonstructural protein NS5
C/Species: Murray Valley encephalitis virus
C/Date: 30-Jun-1988 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
C/Accession: A24635; A60288
R/Dalgarno, L.; Trent, D.W.; Strauss, J.H.; Rice, C.M.
J. Mol. Biol. 187, 309-323, 1986
A/Title: Partial nucleotide sequence of the Murray Valley encephalitis virus genome: C.
A/Reference number: A24635; MUID:86200215; PMID:3009829
A/Accession: A24635
A/Molecule type: Genomic RNA
A/Residues: 1-1780 <DAL>
A/Cross-references: GB:X03467; NID:g59329; PIDN:CNA27184.1; PID:g755731
R/Lee, E.; Fernon, C.; Simpson, R.; Weir, R.C.; Rice, C.M.; Dalgarno, L.
Virus Genes 4, 197-213, 1990
A/Title: Sequence of the 3' half of the Murray Valley encephalitis virus genome and map.
A/Reference number: A60288; MUID:91102934; PMID:1702914
A/Accession: A60288
A/Molecule type: Genomic RNA
A/Residues: 1504-1778, 'V', 1780-3434 <LEE>

C;Superfamily: yellow fever virus genome polyprotein
 C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
 F:1-125/Product: capsid protein #status predicted <CAP>
 F:126-292/Product: membrane protein precursor #status predicted <GLC>
 F:126-217/Domain: nonterminal signal sequence #status predicted <SIG>
 F:218-292/Product: membrane protein #status predicted <GLM>
 F:218-292/Domain: transmembrane #status predicted <TN1>
 F:293-793/Product: envelope protein #status predicted <ENV>
 F:773-793/Domain: transmembrane #status predicted <TN2>
 F:794-1205/Product: nonstructural protein NS1 #status predicted <NS1>
 F:1206-1372/Product: nonstructural protein NS2a #status predicted <NS2a>
 F:1373-1503/Product: nonstructural protein NS2b #status predicted <NS2b>
 F:1504-2122/Product: nonstructural protein NS3 #status predicted <NS3>
 F:1697-1704/Region: nucleotide-binding motif A (P-loop)
 F:1784-1789/Region: nucleotide-binding motif B
 F:1788-1791/Region: DRAB motif
 F:2123-2414/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:2415-2529/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2530-3434/Product: nonstructural protein NS5 #status predicted <NS5>
 F:73.140.446/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.5%; Score 7; DB 1; Length 3434;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VFTVLL 26
 |||||
 DB 278 VFTVLL 284

RESULT 46
 T04365
 ethylene responsive element binding protein - rice
 C;Species: Oryza sativa (rice)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
 R;Kim, C.Y.; Jeong, M.S.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
 submitted to the EMBL Data Library, March 1997
 A;Description: Isolation and characterization of early inducible rice genes by a fungal
 A;Reference number: Z15314
 A;Accession: T04365
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-47 <KIM>
 A;Cross-references: EMBL:U95216; NID:G2443456; PIDN:AAB71382.1; PID:G2443457
 C;Genetics:
 A;Gene: EREBP1

Query Match 2.1%; Score 6; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSL 29
 |||||
 DB 2 VLLQSL 7

RESULT 47
 S78202
 H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - fission yeast (Schizosacchar
 C;Species: mitochondrion Schizosaccharomyces pombe
 C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
 R;Lang, B.F.
 submitted to the EMBL Data Library, August 1990
 A;Description: The mitochondrial genome of the fission yeast Schizosaccharomyces pombe:
 chizosaccharomyces pombe and Aspergillus nidulans.
 A;Reference number: S78195
 A;Accession: S78202
 A;Molecule type: DNA
 A;Residues: 1-48 <LAN>
 A;Cross-references: EMBL:X54421; NID:G13639; PID:G1334456
 A;Experimental source: strain ad7-50h

C;Genetics:
 A;Gene: atp8
 A;Genome: mitochondrion
 A;Genetic code: SGC2
 C;Superfamily: yeast H+-transporting ATP synthase protein 8
 C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; ox

Query Match 2.1%; Score 6; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 IFTVLL 26
 |||||
 DB 19 IFTVLL 24

RESULT 48
 AF2105
 hypothetical protein asl2397 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AF2105
 R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AF2105
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-55 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BA74096.1; PID:G17131489; GSPDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: asl2397

Query Match 2.1%; Score 6; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 FLSNLH 168
 |||||
 DB 35 FLSNLH 40

RESULT 49
 C60157
 hypothetical protein 2 (prtM 5' region) - Lactococcus lactis subsp. cremoris plasmid pW
 C;Species: Lactococcus lactis subsp. cremoris
 C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 03-Feb-2003
 C;Accession: C60157
 R;Haandrikman, A.J.; van Leeuwen, C.; Kok, J.; Vos, P.; de Vos, W.M.; Venema, G.
 Appl. Environ. Microbiol. 56, 1890-1896, 1990
 A;Title: Insertion elements on lactococcal proteinase plasmids.
 A;Reference number: A60157; MUID:90343335; PMID:2166472
 A;Accession: C60157
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-56 <HAA>
 A;Cross-references: GB:M37396; NID:G149472; PIDN:AAA25212.1; PID:G149474
 C;Genetics:
 A;Genome: plasmid pW05

Query Match 2.1%; Score 6; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSL 29
 |||||
 DB 39 VLLQSL 44

```
RESULT 50
C97621
hypothetical protein AGR_C3957 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: C97621
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21609551; PMID:11743194
A:Accession: C97621
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK87924.1; PID:gl5157324; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C3957
A:Map position: circular chromosome

Query Match          2.1%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 GPQRVA 123
Db 7 GPQRVA 12

RESULT 51
AG0025
probable bacterioferritin-associated ferredoxin bfd [imported] - Yersinia pestis (strain
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C:Accession: AG0025
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0025
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-64 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89066.1; PID:gl5978306; GSPDB:GN00175
C:Genetics:
A:Gene: bfd
C:Superfamily: yheA protein

Query Match          2.1%; Score 6; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLROLV 88
Db 28 QLROLV 33

RESULT 52
AC0774
hypothetical protein STY2363 [imported] - Salmonella enterica subsp. enterica serovar Ty
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0774
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gara, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
```

```
A:Accession: AC0774
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-65 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02513.1; PID:gl503375; GSPDB:GN00176
C:Genetics:
A:Gene: STY2363

Query Match          2.1%; Score 6; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 IKENTK 201
Db 46 IKENTK 51

RESULT 53
C91249
hypothetical protein ECs4963 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: C91249
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91249
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-85 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAH38386.1; PID:gl3364439; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs4963

Query Match          2.1%; Score 6; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 EKOQNI 110
Db 31 EKOQNI 36

RESULT 54
S78744
protein YDR363w-a - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 19-Apr-2002
C:Accession: S78744
R:Du, Z.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of S. cerevisiae cosmid 9476.
A:Reference number: S61148
A:Accession: S78744
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <DUZ>
A:Cross-references: EMBL:U28372; MIPS:YDR363w-a
C:Genetics:
A:Gene: SGD:HOD1
A:Cross-references: SGD:S0007235
A:Map position: 4R

Query Match          2.1%; Score 6; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 FTMELK 43
Db 73 FTMELK 78
```

RESULT 55
B82311
conserved hypothetical protein VC0527 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: B82311
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charadon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82311
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <HEI>
A:Cross-references: GB:AE004139; GB:AE003852; NID:G9654953; PIDN:AAF93695.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0527
A:Map position: 1
C:Superfamily: hypothetical protein HI0673

Query Match 2.1%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 NLHLRN 171
|||||
Db 47 NLHLRN 52

RESULT 56
AE3205
transposase tnp [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont) plasmid AT
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AE3205
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2322, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <KUR>
A:Cross-references: GB:AE008687; PIDN:AAL46059.1; PID:gl7743819; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: tnp
A:Genome: Plasmid

Query Match 2.1%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 LVRERG 118
|||||
Db 17 LVRERG 22

RESULT 57
G91248
hypothetical protein ECs4959 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C:Species: *Escherichia coli*
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: G91248

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G91248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA038382.1; PID:gl3364435; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs4959

Query Match 2.1%; Score 6; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 SFGCAF 278
|||||
Db 15 SFGCAF 20

RESULT 58
C95337
probable cytochrome C fragment [imported] - *Sinorhizobium meliloti* (strain 1021) magapl
C:Species: *Sinorhizobium meliloti*
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: C95337
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium melilo*
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95337
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <KUR>
A:Cross-references: GB:AB006469; PIDN:AAK65261.1; PID:gl4523712; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMal13
A:Genome: plasmid

Query Match 2.1%; Score 6; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 VAAHIT 127
|||||
Db 96 VAAHIT 101

RESULT 59
E69832
conserved hypothetical protein yhg8 - *Bacillus subtilis*
N:Alternate names: hypothetical protein y (pbpF 5' region)
C:Species: *Bacillus subtilis*
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: E69832; C40614
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallego, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koether, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.P.; Zunsstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69832
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-104 <KUN>
A;Cross-references: GB:299109; GB:AL009126; NID:G2633260; PIDN:CAB12849.1; PID:ell83011;
A;Experimental source: strain 168
R;Popham, D.L.; Setlow, P.
J. Bacteriol. 175, 4870-4876, 1993
A;Title: Cloning, nucleotide sequence, and regulation of the *Bacillus subtilis* pbpF gene
A;Reference number: A40614; MUID:93328693; PMID:8335642
A;Accession: C40614
A;Molecule type: DNA
A;Residues: 1-57 <POP>
A;Cross-references: GB:LI0630
C;Genetics:
A;Gene: yhgB

Query Match 2.1%; Score 6; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 LMKSR 227
Db 25 LMKSR 30

RESULT 60
B86818
hypothetical protein YpiJ [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C;Species: *Lactococcus lactis* subsp. *lactis*
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: B86818
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: B86818
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <STO>
A;Cross-references: GB:AE005176; PID:g12724547; PIDN:AAK05644.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: YpiJ

Query Match 2.1%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 SSPNSK 142
Db 42 SSPNSK 47

RESULT 61
S09964
Ig kappa chain V-J region (105-2H) - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: S09964
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jatou, J.C.; Izui, S.

Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibod
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09964
A;Molecule type: mRNA
A;Residues: 1-107 <REI>
A;Cross-references: EMBL:X51852; NID:g55393; PIDN:CAA36145.1; PID:g930229
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 2.1%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 TISTVQ 104
Db 74 TISTVQ 79

RESULT 62
A44887
Glucose transporter isoform 1, GLUT 1 - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 24-Sep-1999
C;Accession: A44887
R;Hogan, A.; Heyner, S.; Charton, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.;
Development 113, 363-372, 1991
A;Title: Glucose transporter gene expression in early mouse embryos.
A;Reference number: A44887; MUID:92111400; PMID:1765007
A;Accession: A44887
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <HOG>
A;Cross-references: GB:S77924; NID:g242127; PIDN:AAB20846.1; PID:g242128
A;Experimental source: embryo
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:77924, NCBIIP:77925)
C;Superfamily: glucose transport protein

Query Match 2.1%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 IFTVLL 26
Db 80 IFTVLL 85

RESULT 63
F84012
hypothetical protein BH2902 [imported] - *Bacillus halodurans* (strain C-125)
C;Species: *Bacillus halodurans*
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F84012
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hi
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* an
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84012
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <STO>
A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA006621.1; GSPDB:GN
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2902

Query Match 2.1%; Score 6; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 RNGLV 175

Db 38 RNGELV 43
|||||

RESULT 64

AC2887 conserved hypothetical protein Atu2526 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AC2887

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Karp, P.; Romero, P.; Zhand, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:21608550; PMID:11743193

A:Accession: AC2887

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: GB:AE008688; PIDN:AAL43513.1; PID:gl7741022; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu2526

A:Map position: circular chromosome

Query Match 2.1%; Score 6; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 HLRNGE 173

|||||

Db 35 HLRNGE 40

RESULT 65

H97662 hypothetical protein AGR_C_4590 [imported] - Agrobacterium tumefaciens (strain C58, Cere)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: H97662

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58

A:Reference number: A97359; PMID:21608551; PMID:11743194

A:Accession: H97662

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK88257.1; PID:gl51517717; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_4590

A:Map position: circular chromosome

Query Match 2.1%; Score 6; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 HLRNGE 173

|||||

Db 35 HLRNGE 40

RESULT 66

B25924 Ig kappa chain precursor V region (Ser-b) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000

C:Accession: B25924

A:Residues: 1-117 <KUR>

R:Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.

Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
A:Title: Structural differences in a single gene encoding the V-kappa-Ser group of light chain (Ser-b) in the mouse immunoglobulin V region (Ser-b) - mouse
A:Reference number: A94141; PMID:87067464; PMID:3097643
A:Accession: B25924

A:Molecule type: DNA

A:Residues: 1-115 <BOY>

A:Cross-references: GB:M14360; NID:gl97464; PIDN:AAA39034.1; PID:gl97465

A:Experimental source: strain BALB/c

C:Genetics:

A:Introns: 17/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V region Ser-b #status predicted <NAT>

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 2.1%; Score 6; DB 2; Length 115;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 TISTVQ 104

|||||

Db 94 TISTVQ 99

RESULT 67

C83166

probable chaperone PA3842 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83166

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lazbig, K.; Lim

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen

A:Reference number: A82950; PMID:20437337; PMID:10984043

A:Accession: C83166

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-116 <STO>

A:Cross-references: GB:AE004801; GB:AE004091; NID:g9950011; PIDN:AAG07229.1; GSPDB:GN00

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA3842

C:Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein syce

Query Match 2.1%; Score 6; DB 2; Length 116;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 PNDEES 72

|||||

Db 21 PNDEES 26

RESULT 68

F97174

hypothetical protein CAC2228 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: F97174

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl.

A:Reference number: A96900; PMID:21359325; PMID:21359325

A:Accession: F97174

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK80185.1; PID:gl5025227; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:
A;Gene: CAC2228

Query Match 2.1%; Score 6; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 NGELVI 176
Db 91 NGELVI 96

RESULT 69

JQ2032
lambda 208 protein - Orgyia pseudotsugata multicausid nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata multicausid nuclear polyhedrosis virus, OpNPV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JQ2032

R;Russell, R.L.Q.; Rohrmann, G.F.

J. Gen. Virol. 74, 1191-1195, 1993
A;Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsugata multicausid nuclear polyhedrosis virus
A;Reference number: PQ0633; MUID:93286576; PMID:8389803

A;Accession: JQ2032

A;Molecule type: DNA

A;Residues: 1-119 <RUS>

A;Cross-references: DBJ:D13375; NID:G222217; PIDN:BAA02641.1; PID:G222223
C;Superfamily: Orgyia pseudotsugata multicausid nuclear polyhedrosis virus lambda 208 pr

Query Match 2.1%; Score 6; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQIV 88
Db 90 QLRQIV 95

RESULT 70

D89803
conserved hypothetical protein SA0358 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D89803

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: D89803

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-122 <KUR>

A;Cross-references: GB:BA000018; PID:G13700285; PIDN:BAB41583.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0358

Query Match 2.1%; Score 6; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KEDDSY 64
Db 42 KEDDSY 47

RESULT 71

AH0043
Probable lipoprotein YPO0352 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AH0043

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Hoiden, M.T.G.; Prentice, M.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11596360

A;Accession: AH0043

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-128 <KUR>

A;Cross-references: GB:AL590842; PIDN:CAC89211.1; PID:G15978450; GSPDB:GN00175

C;Genetics:

A;Gene: YPO0352

C;Superfamily: Escherichia coli hypothetical protein ol28

Query Match 2.1%; Score 6; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 SNTLSS 138
Db 35 SNTLSS 40

RESULT 72

D64559
hypothetical protein HP0316 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C;Accession: D64559

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: D64559

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-130 <TOM>

A;Cross-references: GB:AE000549; GB:AE000511; NID:G2313403; PIDN:AA007385.1; PID:G2313

Query Match 2.1%; Score 6; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 FTNELK 43
Db 111 FTNELK 116

RESULT 73

F86829
ribose ABC transporter permease protein rbsd [imported] - Lactococcus lactis subsp. la
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: F86829

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehr
Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: F86829

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <STO>

A;Cross-references: GB:AE005176; PID:G12724648; PIDN:AAK05736.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: rbsd

C;Superfamily: fucose operon U protein

Query Match 2.1%; Score 6; DB 2; Length 132;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 EEIKEN 199
DB 71 EEIKEN 76

RESULT 74

F70650
hypothetical protein Rv3069 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: F70650
R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70650
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-132 <COL>
A;Cross-references: GB:Z83866; GB:AL123456; NID:g3261691; PIDN:CAB06254.1; PID:gi1781144
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv3069
C;Superfamily: hypothetical protein MJ1523

Query Match 2.1%; Score 6; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GAFLVG 281
DB 48 GAFLVG 53

RESULT 75

AC0855
probable regulatory protein STY3045 [imported] - Salmonella enterica subsp. enterica serotype
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0855
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, R.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0855
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06026.1; PID:gi6503993; GSPDB:GN00176
C;Genetics:
A;Gene: STY3045

Query Match 2.1%; Score 6; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QLVRYM 91
DB 127 QLVRYM 132

Search completed: March 23, 2004, 09:24:14
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:16:30 ; Search time 18 seconds
(without alignments)
812.873 Million cell updates/sec

Title: US-10-662-429-2
Perfect score: 281
Sequence: 1 MANMEVGGPSLGTCTLV.....NEHLMDHEASFFGAFLVG 281

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	1	TN10_HUMAN
2	14	5.0	291	1	TN10_MOUSE
3	7	2.5	51	1	INS_ORNAN
4	7	2.5	81	1	VMD2_MOUSE
5	7	2.5	96	1	AH4_TOXGO
6	7	2.5	204	1	LIPE_NITEU
7	7	2.5	209	1	GEMI_HUMAN
8	7	2.5	240	1	CD7_HUMAN
9	7	2.5	362	1	YELJ_CABEL
10	7	2.5	420	1	SUN4_YEAST
11	7	2.5	442	1	MNTH_ANASP
12	7	2.5	475	1	UAP1_SCHPO
13	7	2.5	554	1	HVES_RAT
14	7	2.5	574	1	C306_DROME
15	7	2.5	670	1	YFGG_SCHPO
16	7	2.5	703	1	AT6B_HUMAN
17	7	2.5	979	1	VGLB_HSVEL
18	7	2.5	982	1	YS96_CABEL
19	7	2.5	1009	1	UVRA_STRAW
20	7	2.5	1014	1	UVRA_STRCO
21	7	2.5	1095	1	AT9B_HUMAN
22	7	2.5	1095	1	AT9B_MOUSE
23	7	2.5	1780	1	POLG_MVEV
24	6	2.1	48	1	ATP8_SCHPO
25	6	2.1	67	1	RL29_METAC
26	6	2.1	67	1	RL29_METAC
27	6	2.1	94	1	FISB_VIBCH
28	6	2.1	96	1	IMMK_ECOLI
29	6	2.1	104	1	YHGB_BACSU
30	6	2.1	119	1	Y13K_NPVP
31	6	2.1	126	1	ACPS_VIBPA
32	6	2.1	132	1	CRB1_MYCTU
33	6	2.1	137	1	YB47_SYNY3

34	6	2.1	143	1	B701_HSV6G
35	6	2.1	152	1	YE81_METJA
36	6	2.1	185	1	YAJ5_SCHPO
37	6	2.1	174	1	TN15_HUMAN
38	6	2.1	181	1	YE18_METJA
39	6	2.1	183	1	NLPC_HAEIN
40	6	2.1	184	1	UBC4_WHEAT
41	6	2.1	190	1	RL9_DROME
42	6	2.1	200	1	COAE_STRCO
43	6	2.1	209	1	GLOB_TOBAC
44	6	2.1	210	1	CYC4_AZOVI
45	6	2.1	220	1	RPOA_ASTLO
46	6	2.1	224	1	THY2_XENLA
47	6	2.1	227	1	THY1_XENLA
48	6	2.1	233	1	HIS9_THEMA
49	6	2.1	235	1	RGSI_HUMAN
50	6	2.1	236	1	UBL1_YEAST
51	6	2.1	238	1	F801_SCHMA
52	6	2.1	245	1	PDXJ_SHEON
53	6	2.1	247	1	THL1_ARATH
54	6	2.1	254	1	PSE3_HUMAN
55	6	2.1	257	1	OXAL_BACHD
56	6	2.1	260	1	FLGG_BUCBP
57	6	2.1	261	1	RL1_HSV2H
58	6	2.1	261	1	TNF5_AOTTR
59	6	2.1	261	1	TNF5_BOVIN
60	6	2.1	261	1	TNF5_CALJA
61	6	2.1	261	1	YKNA_CLOSA
62	6	2.1	262	1	CTE2_HUMAN
63	6	2.1	262	1	CTE2_MOUSE
64	6	2.1	262	1	YA23_METJA
65	6	2.1	267	1	YKU6_YEAST
66	6	2.1	272	1	TNF5_CHICK
67	6	2.1	273	1	DEFC_ARATH
68	6	2.1	279	1	DEFC_LYCES
69	6	2.1	282	1	KC2C_ARATH
70	6	2.1	283	1	DPH5_SCHPO
71	6	2.1	284	1	YNFH_ECOLI
72	6	2.1	285	1	LPXC_CHLVC
73	6	2.1	288	1	YHCS_HAEIN
74	6	2.1	291	1	EGCI_LISIN
75	6	2.1	291	1	EGCI_LISMO
76	6	2.1	296	1	NIH2_ANAVA
77	6	2.1	297	1	PANE_LISMO
78	6	2.1	299	1	Y025_MYCPN
79	6	2.1	304	1	XERD_COREF
80	6	2.1	306	1	PERE_ARMRU
81	6	2.1	307	1	YL72_ARCFU
82	6	2.1	313	1	YM58_YEAST
83	6	2.1	313	1	YM8C_YEAST
84	6	2.1	318	1	Y940_METJA
85	6	2.1	319	1	YQAU_BACSU
86	6	2.1	322	1	FATB_VIBAN
87	6	2.1	322	1	YKCC_BACSU
88	6	2.1	323	1	YKCC_BACSU
89	6	2.1	327	1	GSPK_ECOLI
90	6	2.1	329	1	YA90_MYCPN
91	6	2.1	329	1	YQGI_CABEL
92	6	2.1	330	1	RXI_ERARE
93	6	2.1	333	1	LDHB_XENLA
94	6	2.1	334	1	T2D5_HAEIN
95	6	2.1	340	1	FMT_SCHPO
96	6	2.1	340	1	ILVC_CAMJE
97	6	2.1	340	1	LEU3_COREF
98	6	2.1	340	1	YF71_ARCFU
99	6	2.1	341	1	VSX1_CARAU
100	6	2.1	342	1	PURS_LACSK

ALIGNMENTS

RESULT 1

TN10 HUMAN
ID TN10 HUMAN STANDARD; PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN TNFSF10 OR TRAIL OR APO2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=961111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis.";
RL Immunity 3:673-682(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96278649; PubMed=8663110;
RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
RA Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family.";
RL J. Biol. Chem. 271:12687-12690(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX MEDLINE=20017054; PubMed=10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed=10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Screaton G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.

MEHLINE=99413670; PubMed=10485660;
RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
RA Sung Y.C., Oh B.-H.;
RT "2.8 Å resolution crystal structure of human TRAIL, a cytokine with
RT selective antitumor activity.";
RL Immunity 11:253-261(1999).
CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC may be modulated by binding to the decoy receptors
CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC induce apoptosis.
CC -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
CC trimer.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
CC AND PROSTATE.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; U37518; AAC50332.1; -;
CC EMBL; U57059; AAB01233.1; -;
CC EMBL; BC032722; AAH32722.1; -;
CC PDB: 1D0G; 22-OCT-99.
CC PDB: 1D4V; 01-NOV-99.
CC PDB: 1D2Q; 11-FEB-00.
CC PDB: 1DG6; 26-SEP-01.
CC Gene; HGNC:11925; TNFSF10.
CC MIM; 603598; -;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005625; C: soluble fraction; TAS.
CC GO; GO:0005102; P: receptor binding; TAS.
CC GO; GO:0007267; P: cell-cell signaling; TAS.
CC GO; GO:0006917; P: induction of apoptosis; TAS.
CC GO; GO:0007165; P: signal transduction; TAS.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF-like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS00049; TNF 2; 1.
CC Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
CC Zinc; 3D-structure.
ET DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
ET TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
ET METAL 39 281 (POTENTIAL).
ET METAL 230 230 EXTRACELLULAR (POTENTIAL).
ET STRAND 123 127
ET TURN 130 131
ET TURN 137 139
ET STRAND 149 150
ET STRAND 163 165
ET STRAND 167 170
ET TURN 171 172
ET STRAND 173 176
ET STRAND 180 193
ET STRAND 205 213
ET STRAND 220 228
ET STRAND 237 250
ET TURN 252 253
ET STRAND 255 260
ET HELIX 263 265

FT STRAND 266 267
 FT TURN 270 272
 FT STRAND 274 281
 SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;
 Query Match 100.0%; Score 281; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.1e-294;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVLIFFVTLQSLQVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGTCLVLIFFVTLQSLQVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDESNMSPQWQVQWQLRQLVRKMLRTSEETISTVQEKQOINSPVLRGPG 120
 DB 61 DDSYWDNDESNMSPQWQVQWQLRQLVRKMLRTSEETISTVQEKQOINSPVLRGPG 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSPFSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSPFSLNHLRNGELVTHEKG 180
 QY 181 FYIYSQYTFRFQBEIKENTKNDKQMVQYIYKITSYDPDPILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQYTFRFQBEIKENTKNDKQMVQYIYKITSYDPDPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFSVTVNEHLMDHDEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFSVTVNEHLMDHDEASFFGAFLVG 281

RESULT 2

INS_ORNAN STANDARD; PRT; 291 AA.
 ID TN10_MOUSE
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 apoptosis inducing ligand) (TNFRL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.
 RT Identification and characterization of a new member of the TNF
 family that induces apoptosis."
 RL Immunity 3:673-682(1995).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: WIDESPREAD.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 CC EMBL; U37522; AAC52345.1; -.

DR HSP; P50591; IDOG.
 DR MGD; MGI:107414; Tnfsf10.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS50049; TNF 2; 1.
 KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 5.0%; Score 14; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKYSYDPDI 220

DB 217 VQYIYKYSYDPDI 230

RESULT 3

INS_ORNAN STANDARD; PRT; 51 AA.
 ID INS_ORNAN
 AC Q9TQY7; Q9TQY8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Insulin.
 GN INS
 OS Ornithorhynchus anatinus (Duckbill platypus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
 OX NCBI_TaxID=9259;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=97021710; PubMed=8868070;
 RA Nourse A., Treacy G.B., Shaw D.C., Jeffrey P.D.;
 RT "Platypus insulin: indications from the amino acid sequence of
 RT significant differences in structure from porcine insulin."
 RL Biol. Chem. Hoppe-Seyler 377:147-153(1996).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC FIR; S63591; S63590.
 DR HSP; P01308; IMHJ.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR PRINTS; PR00277; INSULINB.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Glucose metabolism.
 FT CHAIN 1 30 INSULIN B CHAIN.
 FT NON_CONS 30 31
 FT CHAIN 31 51 INSULIN A CHAIN.
 FT DISULFID 7 37 INTERCHAIN.
 FT DISULFID 19 50 INTERCHAIN.
 FT DISULFID 36 41
 SQ SEQUENCE 51 AA; 5854 MW; 0E4D30265D77EAA3 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.3;

```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 178 EKGFFYY 184
DB 21 EKGFFYY 27

RESULT 4
VMD2 MOUSE
ID VMD2 MOUSE STANDARD; PRT; 81 AA.
AC O88870;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bestrophin 1 (Vitelliform macular dystrophy protein 2 homolog)
DE (Fragment)
GN VMD2 OR BMD1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98324772; PubMed=9662395;
RA Petukhin K., Kolsti M.G., Bakali B., Li W., Xie G., Marknell T.,
RA Sandgren O., Forsman K., Holmgren G., Andreasson S., Vujic M.,
RA Bergen A.A., McGarty-Dugan V., Figueroa D., Austin C.P., Metzker M.L.,
RA Caskey C.T., Wadelius C.;
RT "Identification of the gene responsible for Best macular dystrophy.";
RT Nat. Genet. 19:241-247(1998).
CC -!- FUNCTION: Forms calcium-sensitive chloride channels. May conduct
CC other physiologically significant anions such as bicarbonate (By
CC similarity).
CC -!- SUBUNIT: Tetramer or pentamers. May interact with PPP2CB and
CC PPP2R1B (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein; plasma membrane.
CC -!- PTM: Phosphorylated by PP2A (By similarity).
CC -!- SIMILARITY: Belongs to the bestrophin family.

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EMBL; AF057171; AAC64345.1; -.
DR MGD; MGI:1346332; Vmd2.
DR GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR InterPro; IPR000615; Bestrophin.
DR Pfam; PF01062; Bestrophin; 1.
DR ProDom; PD002802; Worm fam.8; 1.
KW Transport; Ion transport; Ionic channel; Chloride channel; Chloride;
KW Calcium; Transmembrane; Phosphorylation.
FT NON_TER 1
FT NON_TER 81
FT NON_TER 81
SQ SEQUENCE 81 AA; 9413 MW; 19FD94AB3D606178 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 TVLLQSL 29
DB 27 TVLLQSL 33

RESULT 5
AH4_TOXGO
ID AH4_TOXGO STANDARD; PRT; 96 AA.
AC Q27001;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Antigen H4 (Fragment).
GN H4.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RX MEDLINE=91216437; PubMed=2022319;
RA Johnson A.M., Iilana S.;
RT "Cloning of Toxoplasma gondii gene fragments encoding diagnostic
RT antigens.";
RT Gene 99:127-132(1991).
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CC
CC EMBL; M57302; AAA30139.1; -.
DR PIR; PS0423; PS0423.
KW Antigen.
FT NON_TER 1
FT CARBOHYD 34
FT CARBOHYD 34
SQ SEQUENCE 96 AA; 10853 MW; 69C7C2D14890FA53 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 192 FOEIKE 198
DB 2 FOEIKE 8

RESULT 6
LIPB NITEU
ID LIPB NITEU STANDARD; PRT; 204 AA.
AC Q82UJ6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipocate-protein ligase B (EC 6.4.1.1) (lipocate biosynthesis protein
DE B).
GN LIPB OR NE1488.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RT J. Bacteriol. 185:2759-2773(2003).
CC -!- FUNCTION: Involved in the attachment of lipoyl groups to proteins,
CC by creating an amide linkage that joins the free carboxyl group of
CC lipolic acid to the epsilon-amino group of a specific lysine
CC residue in lipoylated proteins (By similarity).
CC -!- PATHWAY: Lipocate biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the lipB family.

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CC -----
 CC EMBL; BX321861; CAD853399.1; -;
 CC HAMAP; MF 00013; -;
 CC InterPro; IPR004143; BLP LipA LipB.
 CC InterPro; IPR000544; Lipocate_B.
 CC Pfam; PF03099; BLP LipA LipB; 1.
 CC ProDom; PD06086; Lipocate_B; 1.
 CC TIGRFAMs; TIGR00214; lipB; 1.
 CC PROSITE; PS01313; lipB; 1.
 CC KW Ligase; Complete proteome.
 CC SEQUENCE 204 AA; 22764 MW; A83F6E5F0346E61 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 RQLVRKM 91

DB 97 RQLVRKM 103.

RESULT 7

GEMI_HUMAN STANDARD; PRT; 209 AA.

AC 075496; QH1Z1;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Geminin.

GN GMIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98297356; PubMed=9635433;

RA McGarry T.J.; Kirschner M.W.;

RT "Geminin, an inhibitor of DNA replication, is degraded during

RT mitosis.";

RL Cell 93:1043-1053 (1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Corby N.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Lung and Urinary bladder;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

RA Klausner R.D.; Collins F.S.; Wagner L.; Schenker C.F.; Bhat N.K.;

RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haieh F.;

RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;

RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

RA Brownstein M.J.; Uedin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;

RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

RA Phay J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;

RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

RA Blakesley R.W.; Touchman J.W.; Schmutz J.; Myers R.M.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smalios D.E.;

RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;

RT

human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Inhibits DNA replication by preventing the incorporation

CC of MCM complex into prereplication complex (pre-RC). It is

CC degraded during the mitotic phase of the cell cycle. Its

CC destruction at the metaphase-anaphase transition permits

CC replication in the succeeding cell cycle.

CC -1- DEVELOPMENTAL STAGE: Absent during G1 phase, accumulates during S,

CC G2, and M phases, and disappears at the time of the metaphase-

CC anaphase transition.

CC -1- SIMILARITY: Belongs to the geminin family.

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CC -----
 CC EMBL; AF067855; AAC39787.1; -;
 CC EMBL; ALJ33264; CAC21511.1; ALT_INIT.
 CC EMBL; BC005185; AAH05185.1; -;
 CC EMBL; BC005389; AAH05389.1; -;
 CC Genew; HGNC:17493; GMIN.

CC GK; 075496; -;

CC GO; GO:0007050; P:cell cycle arrest; TAS.

CC GO; GO:0008156; P:negative regulation of DNA replication; TAS.

CC Cell cycle.

CC SEQUENCE 209 AA; 23565 MW; 0BABE60F6F5AC252 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 209;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199

DB 9 QEEIKEN 15

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF 205-240 FROM N11.
RX MEDLINE=91267564; PubMed=1711009;
RA Yoshikawa K., Seto M., Ueda R., Notake K., Yokochi T.,
RA Takahashi T.;
RT "Molecular cloning of the gene coding for the human T cell
RT differentiation antigen CD7.";
RL Immunogenetics 33:352-360 (1991).
RN [5]
RP TOPOLOGY.
RX MEDLINE=90063052; PubMed=2479685;
RA Ware R.E., Scarce R.M., Dietz M.A., Starmer C.F., Palke T.J.,
RA Haynes B.F.;
RT "Characterization of the surface topography and putative tertiary
RT structure of the human CD7 molecule.";
RL J. Immunol. 143:3632-3640 (1989).
RN [6]
RP INTERACTION WITH SECTM1.
RX MEDLINE=20119303; PubMed=10652336;
RA Lyman S.D., Escobar S., Rousseau A.-M., Armstrong A., Fanslow W.C.;
RT "Identification of CD7 as a cognate of the human K12 (SECTM1)
RT protein.";
RL J. Biol. Chem. 275:3431-3437 (2000).
CC -!- FUNCTION: Not yet known.
CC -!- SUBUNIT: Interacts with SECTM1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD7 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd7.htm".
CC -----
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CC -----
DR EMBL; X06180; CRA29546.1; -
DR EMBL; M37271; AAA51953.1; -
DR EMBL; BC009293; AAH09293.1; -
DR EMBL; BC013297; AAH13297.1; -
DR EMBL; D00749; BAA00646.1; -
DR EMBL; D00747; BAA00646.1; JOINED.
DR EMBL; D00748; BAA00646.1; JOINED.
DR F01; A39016; A39016.
DR HSP; P01607; IREI.
DR Genew; HGNC:1695; CD7.
DR MIM; 168620; -
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0006955; P:immune response; TAS.
GO; GO:0042110; P:T-cell activation; TAS.
GO; GO:0007159; P:transmembrane receptor protein tyrosine kin. .; NAS.
InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
T-cell; Signal; Immune response; Antigen; Transmembrane; Glycoprotein;
Immunoglobulin domain; Receptor; Lipoprotein; Palmitate; Repeat.
FT CHAIN 1 25
FT SIGNAL 26 240
FT DOMAIN 26 180
FT TRANSMEM 181 201
FT DOMAIN 202 240
FT DOMAIN 26 130
FT DOMAIN 145 180
FT DISULFID 35 142
FT DISULFID 48 114
FT LIPID 198 198
FT CARBOHYD 45 45
FT CARBOHYD 96 96
FT REPEAT 145 153
FT REPEAT 154 162
FT REPEAT 163 171
FT REPEAT 172 180
SQ SEQUENCE 240 AA; 25409 MW; EBBCE08279552108 CRC64;
Query Match 2.5%; Score 7; DB 1; Length 240;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 134 NTLSSPN 140
Db 231 NTLSSPN 237

RESULT 9
YELJ CABEL
ID YELJ CABEL STANDARD; PRT; 362 AA.
AC P90756;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C27A7.2 in chromosome V.
GN C27A7.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Harris B.R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RN REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE DUF23 FAMILY.
CC -----
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CC -----
DR EMBL; Z81041; CAB02786.2; -
DR WormPep; C27A7.2; CE31886.
DR InterPro; IPR006166; DUF23.


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DR Pfam; PF01566; N-ramp; 1.
DR PRINTS; PR00447; NATRESASCOMP.
DR ProDom; PD001861; N-ramp; 1.
DR TIGRFAMs; TIGR011197; n-ramp; 1.
KW Transport; Symport; Manganese; Transmembrane; Inner membrane; Plasmid;
KW Complete proteome.
FT TRANSMEM 29 49 POTENTIAL.
FT TRANSMEM 62 82 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 258 278 POTENTIAL.
FT TRANSMEM 295 315 POTENTIAL.
FT TRANSMEM 347 367 POTENTIAL.
FT TRANSMEM 372 392 POTENTIAL.
FT TRANSMEM 413 433 POTENTIAL.
SQ SEQUENCE 442 AA; 48418 MW; A7CBADFAE628196B CRC64;

Query Match 2.5%; Score 7; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 LIQSLCV 31
DB 76 LIQSLCV 82

RESULT 12
UAP1 SCHPO
ID UAP1 SCHPO STANDARD; PRT; 475 AA.
AC 094617;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23).
GN SPBCL289.08
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy I., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz B.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares K., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RC Nature 415:871-880(2002).
CC -!- CATALYTIC ACTIVITY: UTP + N-acetyl-alpha-D-glucosamine 1-phosphate

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CC = diphosphate + UDP-N-acetyl-D-glucosamine.
CC -!- PATHWAY: UDP-GlcNAc biosynthesis from Fru-6-P; fourth (last)
CC step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -----
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CC -----
CC EMBL; AL035675; CAB38688.1; -
CC PIR; T39359; T39359.
CC GeneDB SPombe; SPBCL289.08; -
CC InterPro; IPR002618; UDPGP.
CC Pfam; PF01704; UDPGP; 1.
CC Transferase; Nucleotidyltransferase.
FT SITE 106 106 BINDING SITE FOR GLCNAC-1-P (BY
FT ACT SITE 110 110 SIMILARITY).
FT ACT SITE 117 117 POTENTIAL.
SQ SEQUENCE 475 AA; 53121 MW; 3AF80295A682D7A3 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 TSEETIS 101
DB 168 TSEETIS 174

RESULT 13
HYES RAT
ID HYES RAT STANDARD; PRT; 554 AA.
AC P80299;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Soluble epoxide hydrolase (SEH) (EC 3.3.2.3) (Epoxide hydratase)
DE Cytosolic epoxide hydrolase (CEH).
DE EPHX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=93352557; PubMed=8349641;
RA Knehr M., Thomas H., Arand M., Gebel T., Zeller H.-D., Oesch F.;
RA "Isolation and characterization of a cDNA encoding rat liver
RA cytosolic epoxide hydrolase and its functional expression in
RA Escherichia coli."
RT J. Biol. Chem. 268:17623-17627(1993).
RL [2]
RP SEQUENCE OF 450-554 FROM N.A., AND PARTIAL SEQUENCE.
RN TISSUE=Liver;
RX MEDLINE=92077134; PubMed=1743286;
RA Arand M., Knehr M., Thomas H., Zeller H.-D., Oesch F.;
RA "An impaired peroxisomal targeting sequence leading to an unusual
RA bicompartamental distribution of cytosolic epoxide hydrolase."
RL FEBS Lett. 294:19-22(1991).
CC -!- FUNCTION: This enzyme acts on epoxides (alkene oxides, oxiranes)
CC and arene oxides. Plays a role in xenobiotic metabolism by
CC degrading potential toxic epoxides. Also determines steady-state
CC levels of physiological mediators.
CC -!- CATALYTIC ACTIVITY: An epoxide + H(2)O = a glycol.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and peroxisomal.
CC -!- INDUCTION: By compounds that cause peroxisome proliferation such

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CC as clofibrate, tiadenol and fenofibrate.
CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Epoxide
CC hydrolase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X65083; CAA46211.1; -
CC EMBL; X60328; CAA42898.1; -
CC PIN; A47503; 14C7503.
CC HSP; P34914; 1CR6.
CC InterPro; IPR000073; A/b hydrolase.
CC InterPro; IPR003089; AB hydrolase.
CC InterPro; IPR000639; Epox hydrolase.
CC InterPro; IPR008402; HAD-SF-IA-V3.
CC InterPro; IPR005833; Hlgnaase/hydrolase.
CC InterPro; IPR005834; Hydrolase.
CC InterPro; IPR000379; Ser esters.
CC Pfam; PF00561; abhydrolase_1.
CC Pfam; PF00702; Hydrolase; 1.
CC PRINTS; PR00111; ABHYDROLASE.
CC PRINTS; PR00412; EPOXYHYDROLASE.
CC PRINTS; PR00413; HADHALOGNASE.
CC TIGRFAMs; TIGR01509; HAD-SF-IA-V3; 1.
CC Hydrolase; Peroxisome; Detoxification;
CC Aromatic hydrocarbons catabolism.
CC ACT_SITE 333 333 BY SIMILARITY.
CC ACT_SITE 495 495 BY SIMILARITY.
CC ACT_SITE 523 523 BY SIMILARITY.
CC ACT_SITE 552 554 BY SIMILARITY.
CC SEQUENCE 554 AA; 62340 MW; 145FDCAS3F592138 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 554;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151
DB 477 KALGRKI 483
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RESULT 14
C306 DROME 2.5%; Score 7; DB 1; Length 574 AA.
ID _C306 DROME STANDARD; PRT; 574 AA.
AC Q3VWR5;
DC ACT_SITE 333 333 BY SIMILARITY.
DC ACT_SITE 495 495 BY SIMILARITY.
DC ACT_SITE 523 523 BY SIMILARITY.
DC ACT_SITE 552 554 BY SIMILARITY.
DE Probable cytochrome P450 306A1 (EC 1.14.-.-) (CYPCCCVIAL).
GN CYP306A1 OR CG6578.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000)
CC -!- FUNCTION: May be involved in the metabolism of insect hormones and
CC in the breakdown of synthetic insecticides (By similarity).
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
CC (Potential).
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
CC EMBL; AE003509; AAF48873.1; -
CC HSP; P00179; 1DT6.
CC FlyBase; FBgn0030948; Cyp306a1.
CC InterPro; IPR001128; Cytochrome_P450.
CC Pfam; PF00067; P450; 1.
CC PRINTS; PR00385; P450.
CC PROSITE; PS00086; CYTOCHROME P450; 1.
CC Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
CC Endoplasmic reticulum; Hypothetical protein.
FT METAL 505 505 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 574 AA; 65177 MW; 9A8A3E1747101700 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 574;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 GGIFELK 251
DB 81 GGIFELK 87
|||||

RESULT 15
ID YFGG SCHPO STANDARD; PRT; 670 AA.
AC O13854; O42840;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Hypothetical serine/threonine-rich protein C19G12.16c in chromosome I
DE precursor.

OS SPAC19G12.16c OR SPAC23A1.01C.

GN Schizosaccharomyces pombe (Pissin yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_taxid=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,

RA Weltjens I., Vantreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesti D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Rayon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovsky G.V., Usery D., Barrell B.G., Nurse P.,

RA "The genome sequence of Schizosaccharomyces pombe";

RL Nature 415:871-880(2002).

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

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CC -----

DR EMBL; Z97209; CAB10128.1; ..

DR EMBL; AL021813; CAJ16975.1; ..

DR GeneDB SPombe; SPAC19G12.16c; ..

KW Hypothetical protein; Glycoprotein; Signal.

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

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FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

FT SIGNAL 1 19

FT CHAIN 20 670

SQ SEQUENCE 670 AA; 68262 MW; 68E8D1CFB855F8A8 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 670;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 EETISTV 103

Db 584 EETISTV 590

RESULT 16

AT6B HUMAN

ID AT6B HUMAN STANDARD; PRT; 703 AA.

AC Q99941; Q13269; Q14343; Q14345; Q99635; Q9H3V9; Q9H3W1;

AC Q9NPL0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cyclic-AMP-dependent transcription factor ATF-6 beta (Activating

DE transcription factor 6 beta) (ATF6-beta) (cAMP responsive element

DE binding protein-like 1) (cAMP response element binding protein-related

DE protein) (Creb-rp) (G13 protein).

GN CREB1 OR G13

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_Taxid=9606;

[1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Tonsil;

RX MEDLINE=96163866; PubMed=8586413;

RA Min J., Shukla H., Kozono H., Bronson S.K., Weissman S.M.,

RA Chaplin D.D.;

RT "A novel Creb family gene telomeric of HLA-DRA in the HLA complex.";

RL Genomics 30:149-156(1995).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97024424; PubMed=8870652;

RA Khanna A., Campbell R.D.;

RT "The gene G13 in the class III region of the human MHC encodes a

RT potential DNA-binding protein.";

RL Biochem. J. 319:81-89(1996).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RA Rowen L., Danks C., Baskin D., Faust J., Loretz C., Ahearn M.E.,

RA Banta A., Schwartz S., Smith T.M., Spies T., Hood L.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97081760; PubMed=8923003;

RA Speck M., Barry F., Miller W.L.;

RT "Alternate promoters and alternate splicing of human tenascin-X, a

RT gene with 5' and 3' ends buried in other genes.";

RL Hum. Mol. Genet. 15:1749-1758(1996).

RN [5]

RP SEQUENCE OF 158-700 FROM N.A.

RA Barlow K.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [6]

RP CHARACTERIZATION.

RX MEDLINE=21157024; PubMed=11256944;

RA Haze K., Okada T., Yoshida H., Yanagi H., Yura T., Negishi M.,

RA Mori K.;

RT "Identification of the G13 (cAMP-response-element-binding

RT transcription factor 6 as a transcriptional activator of the

RT mammalian unfolded protein response.";

RL Biochem. J. 355:19-28(2001).

CC -!- FUNCTION: TRANSCRIPTIONAL FACTOR THAT ACTS IN THE UNFOLDED PROTEIN

CC RESPONSE (UPR) PATHWAY BY ACTIVATING UPR TARGET GENES INDUCED

CC DURING ER STRESS. BINDS DNA ON THE 5'-CCAC[GA]-3' HALF OF THE ER

CC STRESS RESPONSE ELEMENT (ERSE) (5'-CCAT-N9-CCAC[GA]-3') WHEN NF-Y


```

QY      52 SGIACTFL 58
Db      |||||
      839 SGIACTFL 845

RESULT 18
YS96_CABEL STANDARD; PRT; 982 AA.
AC Q09965;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative G protein-coupled receptor B0244.6.
GN B0244.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Favello A.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Subfamily B0244.
CC -----
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CC -----
CC EMBL; U28971; AAA68379.1; -.
CC PIR; E88465; E88465.
CC WormPep; B0244.6; C501753.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC KW Hypothetical protein; G-protein coupled receptor; Transmembrane;
CC Glycoprotein.
CC FT TRANSMEM 55 75 POTENTIAL.
CC FT TRANSMEM 87 107 POTENTIAL.
CC FT TRANSMEM 208 228 POTENTIAL.
CC FT TRANSMEM 386 406 POTENTIAL.
CC FT TRANSMEM 430 450 POTENTIAL.
CC FT TRANSMEM 481 501 POTENTIAL.
CC FT TRANSMEM 648 668 POTENTIAL.
CC FT TRANSMEM 693 713 POTENTIAL.
CC FT TRANSMEM 813 833 POTENTIAL.
CC FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 982 AA; 110441 MW; 4E88D46CB74C940E CRC64;

Query Match 2.5%; Score 7; DB 1; Length 982;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      132 RSNTLSL 138
Db      |||||
      461 RSNTLSL 467

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RESULT 19
UVRA_STRAW STANDARD; PRT; 1009 AA.
AC Q829X3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE UVrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
GN UVRA OR SAV6286.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
CC -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC processing of DNA lesions. UvrA is an ATPase and a DNA-binding
CC protein. A damage recognition complex composed of 2 uvrA and 2
CC uvrB subunits scans DNA for abnormalities. When the presence of a
CC lesion has been verified by uvrB, the uvrA molecules dissociate
CC (By similarity).
CC -!- SUBUNIT: Forms a heterotetramer with uvrB during the search for
CC lesions (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
CC -----
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CC -----
CC EMBL; AP005046; BAC73997.1; -.
CC HAMAP; MF 00205; -.
CC InterPro; IPR003439; ABC transporter.
CC InterPro; IPR000345; CytC_heme_BS.
CC InterPro; IPR004602; UvrA.
CC Pfam; PF00005; ABC_tran; 2.
CC ProDom; PD000006; ABC transporter; 1.
CC TIGRFAMs; TIGR00630; uvrA; 1.
CC PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
CC PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
CC SOS response; Excision nuclease; DNA repair; DNA recombination;
CC DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
CC Zinc-finger; Complete proteome.
CC FT NP_BIND 32 39 ATP (POTENTIAL).
CC FT NP_BIND 645 652 ATP (POTENTIAL).
CC FT ZN_FING 744 770 C4-TYPE.
CC SEQUENCE 1009 AA; 110786 MW; CC90B4E219139700 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 1009;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117

Db 153 SPLVRER 159

RESULT 20

UVRA STRCO STANDARD; PRT; 1014 AA.

AC Q92507;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UVABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
GN UVRA OR SC01958 OR SCC54.18C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Thomson N.R., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).

CC -1- FUNCTION: The UvrABC repair system catalyzes the recognition and
processing of DNA lesions. UvrA is an ATPase and a DNA-binding
protein. A damage recognition complex composed of 2 uvrA and 2
uvrB subunits scans DNA for abnormalities. When the presence of a
lesion has been verified by uvrB, the uvrA molecules dissociate
(By similarity).
CC -1- SUBUNIT: Forms a heterotrimer with uvrB during the search for
lesions (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.

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CC -----
CC EMBL; AL939110; CAB38148.1; -.
CC PIR; T36031; -; 1.
CC HMAP; MF_0205; -; 1.
CC InterPro; IPR003439; ABC_transporter.
CC InterPro; IPR004602; UvrA.
CC Pfam; PF00005; ABC_tran; 2.
CC ProDom; PD000006; ABC_transporter; 1.
CC TIGRfams; TIGR00630; UvrA_1.
CC PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
CC PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
CC SOS response; Excision nuclease; DNA repair; DNA recombination;
CC DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
CC Zinc-finger; Complete proteome.
CC NP_BIND 32 39 ATP (POTENTIAL).
CC NP_BIND 645 652 ATP (POTENTIAL).
CC ZN_FING 744 770 C4-TYPE.
CC SEQUENCE 1014 AA; 110997 MW; 084D6B18692A792D CRC64;

Query Match 2.5%; Score 7; DB 1; Length 1014;

RESULT 21

AT9B HUMAN STANDARD; PRT; 1095 AA.

AC O43861; O60872;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1) (HUSSY-
20).
GN ATP9B OR ATP11B OR NEOL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-420 FROM N.A.
RC TISSUE=Testis;
RA Oshina A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Muraashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC [2]
CC SEQUENCE OF 208-1095 FROM N.A.
CC Birren B., Linton L., Nussbaum C., Lander E., Ali A., Allen N.,
CC Anderson S., Barna N., Bastien V., Boguslavskiy L., Boukhgalter B.,
CC Brown A., Camarata J., Campopiano A., Chang J., Chazaro B.,
CC Choepel Y., Collangelo M., Collins S., Collymore A., Cook A., Cooke P.,
CC DeArrellano K., Dewar K., Diaz J.S., Dodge S., Faro S., Ferreira P.,
CC Fitzhugh W., Gage D., Galagan J., Gardyna S., Ginde S., Gord S.,
CC Goyette M., Graham L., Grand-Pierre N., Hagos B., Heaford A.,
CC Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,
CC Karatas A., Kells C., LaRoque K., Lamazares R., Landers T.,
CC Lehoczy J., Levine R., Liu G., MacLean C., Macdonald P., Major J.,
CC Marquis N., Matthews C., McCarthy M., McEwan P., McKernan K.,
CC McPheeters R., Meldrim J., Meneus L., Mihova T., Mienga V., Murphy T.,
CC Naylor J., Nguyen C., Norbu C., Norman C.H., O'Connor T.,
CC O'Donnell P., O'Neill D., Oliver J., Peterson K., Phunkhang P.,
CC Pierre N., Pollara V., Raymond C., Retta R., Rieback M., Riley R.,
CC Rise C., Rogov P., Roman J., Rosetti M., Roy A., Santos R.,
CC Schauer S., Schuback R., Seaman S., Severy P., Spencer B.,
CC Strange-Thomann N., Stojanovic N., Strauss N., Subramanian A.,
CC Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Travis N.,
CC Trigilio J., Vassiliev H., Viel R., Vo A., Wilson B., Wu X., Wyman D.,
CC Ye W.J., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC [3]
CC SEQUENCE OF 759-1095 FROM N.A.
CC TISSUE=Brain;
CC MEDLINE=98217376; PubMed=9548971;
CC Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
CC Schlegel R.A.;
CC "Multiple members of a third subfamily of P-type ATPases identified by
CC genomic sequences and ESTs";
CC Genome Res. 8:354-361(1998).
CC [4]
CC SEQUENCE OF 768-1095 FROM N.A.
CC TISSUE=Brain;
CC MEDLINE=21064499; PubMed=11124703;
CC Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
CC Cannata N., Zimbello R., Lanfranchi G., Valle G.;

"Characterization of 16 novel human genes showing high similarity to yeast sequences";
 Yeast 18:69-80(2001).
 [5]
 RN CONCEPTUAL TRANSLATION.
 RP Axelsson K.B.;
 RL Unpublished Observations (JUL-2002).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
 CC -----
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 CC -----
 CC EMBL; AK097757; -; NOT ANNOTATED_CDS.
 DR EMBL; AC104423; -; NOT ANNOTATED_CDS.
 DR EMBL; U78978; AAC05243.1; -;
 DR EMBL; AJ006268; CAA06934.1; -;
 DR Genew; HGNC:13541; ATP9B.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0015247; F:aminophospholipid transporter activity; NAS.
 DR GO; GO:0005524; F:ATP binding; NAS.
 DR GO; GO:0019829; P:cation-transporting ATPase activity; NAS.
 DR GO; GO:0015917; P:aminophospholipid transport; NAS.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006539; Flippase.
 DR PRINTS; PR00119; CATATPASE.
 DR TIGRFAWS; TIGR01652; ATPase-Pilpid; 1.
 DR PROSITE; PS00154; ATPase_E1_E2; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KW Multigene family.
 FT DOMAIN 1 94
 FT TRANSMEM 95 116
 FT DOMAIN 117 121
 FT TRANSMEM 122 144
 FT DOMAIN 145 328
 FT TRANSMEM 329 349
 FT DOMAIN 350 357
 FT TRANSMEM 358 379
 FT DOMAIN 380 878
 FT TRANSMEM 879 899
 FT DOMAIN 900 911
 FT TRANSMEM 912 930
 FT DOMAIN 931 960
 FT TRANSMEM 961 979
 FT DOMAIN 980 986
 FT TRANSMEM 987 1009
 FT DOMAIN 1010 1015
 FT TRANSMEM 1016 1036
 FT DOMAIN 1037 1053
 FT TRANSMEM 1054 1078
 FT DOMAIN 1079 1095
 FT MOD_RES 416 416
 FT METAL 822 822
 FT METAL 826 826
 FT CONFLICT 834 834
 FT CONFLICT 954 954
 FT CONFLICT 968 968
 FT CONFLICT 984 984
 FT CONFLICT 1021 1021
 FT CONFLICT 1043 1043
 FT CONFLICT 1051 1051
 FT CONFLICT 1079 1079
 FT SEQUENCE 1095 AA; 123635 MW; 570C2E7DE507C255 CRC64;
 Query Match 2.5%; Score 7; DB 1; Length 1095;
 Best Local Similarity 100.0%; Pred. No. 58;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 241 SIYQGGI 247
 DB 968 SIYQGGI 974
 RESULT 22
 AT9B MOUSE
 ID AT9B MOUSE STANDARD; PRT; 1095 AA.
 AC P98155; O59L13;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1).
 GN ATP9B.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 EX MEDLINE=20473714; PubMed=11015572;
 RA Halleck M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P.,
 RA Hacker C., Pyle S., Newman J.F., Nakanishi Y., Ando H., Weinstein D.,
 RA Williamson P., Schlegel R.A.;
 RT "Differential expression of putative transbilayer amphipath
 RT transporters";
 RL Physiol. Genomics 1:139-150(1999).
 RN [2]
 RP SEQUENCE OF 658-1095 FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Found in most tissues except spleen and
 CC muscle. Most abundant in testis. Also detected in fetal tissues.
 CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
 CC ATPases). Subfamily IV.
 CC -----
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 CC -----
 CC EMBL; AF155913; AF08476.1; -;
 DR EMBL; BC003246; AA03246.1; -;
 DR MGD; MGI:1354757; At9b.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR008250; E1-E2_ATPase_reg.


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FT DISULFID 295 322 BY SIMILARITY.
FT DISULFID 352 408 BY SIMILARITY.
FT DISULFID 366 397 BY SIMILARITY.
FT DISULFID 384 413 BY SIMILARITY.
FT DISULFID 482 580 BY SIMILARITY.
FT DISULFID 597 628 BY SIMILARITY.
FT DISULFID 797 808 BY SIMILARITY.
FT DISULFID 848 936
FT DISULFID 972 1016
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 968 968 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1000 1000 N-LINKED (GLCNAC. .) (HIGH MANNOSE).
FT NON_TER 1780 1780
SQ SEQUENCE 1780 AA; 194866 MW; 0D6AA7FF0FB706DE CRC64;

Query Match 2.5%; Score 7; DB 1; Length 1780;
Best Local Similarity 100.0%; Pred.No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVLL 26
DB 278 VIFTVLL 284

RESULT 24
ATP8_SCHPO
ID ATP8 SCHPO STANDARD; PRT; 48 AA.
AC P21536; Q9UUV72;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN ATP8.
OS Schizosaccharomyces pombe (Fission yeast).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD7-50;
RA Lang B.F.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-43 FROM N.A.
RC STRAIN=968 h90;
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hirooka Y.;
RT "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
CC -!- FUNCTION: This is one of the chains of the nonenzymatic component (CF0) subunit of the mitochondrial ATPase complex.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: Belongs to the ATPase protein 8 family.
CC
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CC
CC EMBL; X54421; CAA38291.1; -.
DR EMBL; AB027775; BAA87079.1; -.

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KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 8 32. POTENTIAL.
SQ SEQUENCE 48 AA; 5636 MW; 36B3BF480A5FE803 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 48;
Best Local Similarity 100.0%; Pred.No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 IFTVLL 26
DB 19 IFTVLL 24

RESULT 25
RL29_METAC
ID RL29 METAC STANDARD; PRT; 67 AA.
AC Q8TRU0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L29P.
GN RPL29P OR MAl079.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=2192760; PubMed=1193238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., Brown A., FitzHugh W., Calvo S., Engels R., Smirnov S., Athnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R., Linton L., McGowan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
RL Genome Res. 12:532-542(2002).
CC -!- SIMILARITY: Belongs to the L29P family of ribosomal proteins.
CC
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CC
CC EMBL; AE010775; AAM04504.1; -.
DR HAVAP; MF_00374; -.
DR InterPro; IPR001854; Ribosomal L29.
DR Pfam; PF00831; Ribosomal L29; 1.
DR TIGRFAMs; TIGR00012; L29; 1.
DR PROSITE; PS00579; RIBOSOMAL L29; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 67 AA; 7612 MW; 232230E101E336B8 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 67;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ILRTSE 97
DB 3 ILRTSE 8

RESULT 26

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RL29 METWA
ID RL29_METWA STANDARD; PRT; 67 AA.
AC Q8PV43;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L29P.
GN RPL29P OR M2131.
OS Methanoscarchina maezi (Methanoscarchina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser A., Baumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanoscarchina maezi: evidence for lateral gene
transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- SIMILARITY: Belongs to the L29P family of ribosomal proteins.
CC -----
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CC -----
CC ENBL; AE013454; ANM31827.1; -.
CC HAMAP; MF 00374; -.
CC InterPro; IPR001854; Ribosomal L29.
CC Pfam; PF00831; Ribosomal L29; 1.
CC TIGRfam; TIGR00012; L29; 1.
CC PROSITE; PS00579; RIBOSOMAL_L29; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 67 AA; 7612 MW; 232324E450A236B8 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ILRTSE 97
Db 3 ILRTSE 8

RESULT 27
FTSB_VIBCH STANDARD; PRT; 94 AA.
AC Q9KUJ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cell division protein ftsB.
GN FTSB OR VC0527.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

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RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae";
RL Nature 406:477-483(2000).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=21980622; PubMed=11972052;
RA Buddelmeijer N., Judson N., Boyd D., Mekalanos J.J., Beckwith J.;
RT "YgbQ, a cell division protein in Escherichia coli and Vibrio
RT cholerae, localizes in codependent fashion with FtsL to the division
RT site.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:6316-6321(2002).
CC -!- FUNCTION: Required for the cell division process.
CC -!- SUBUNIT: May interact with FtsL (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
CC (potential). Colocalizes with ftsL to the division site (By
CC similarity).
CC -!- SIMILARITY: Belongs to the ftsB family.
CC -----
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CC -----
CC ENBL; AS004139; AAF93695.1; ALT_INIT.
CC PIR; B82311; B82311.
CC TIGR; VC0527; -.
CC HAMAP; MF 00599; -.
CC InterPro; IPR007060; DivIC.
CC Pfam; PF04977; DivIC; 1.
KW Cell division; Transmembrane; Inner membrane; Coiled coil;
KW Complete proteome.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 21 POTENTIAL.
FT DOMAIN 22 94 PERIPLASMIC (POTENTIAL).
FT DOMAIN 32 76 COILED COIL (POTENTIAL).
SQ SEQUENCE 94 AA; 10987 MW; CE7DF6651369821D CRC64;

Query Match 2.1%; Score 6; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 NLHLRN 171
Db 45 NLHLRN 50

RESULT 28
IMWK_ECOLI STANDARD; PRT; 96 AA.
AC Q47503; Q46784; Q47501;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Colicin K immunity protein.
GN CKI OR CFI.
OS Escherichia coli.
OG Plasmid ColK-K235.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K49, and ECORS;
RX MEDLINE=96074330; PubMed=7592493;
RA Pilel H., Braun V.;
RT "Strong function-related homology between the pore-forming colicins K

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RT J. Bacteriol. 177:6973-6977 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Izard J., Chartier M., Baty D.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: THIS PROTEIN IS ABLE TO PROTECT A CELL, WHICH HARBORS
CC THE PLASMID COLK ENCODING COLICIN K, AGAINST COLICIN K.
CC
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CC
DR EMBL; X87834; CA61100.1; -
DR EMBL; X87835; CA61103.1; -
DR EMBL; U27452; A841289.1; -
KW Bacteriocin immunity; Plasmid; Transmembrane; Inner membrane.
FT TRANSMEM 73 POTENTIAL.
SQ SEQUENCE 96 AA; 11498 MW; E828532395957A5CD CRC64;

Query Match 2.1%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 IKENTK 201
DB 55 IKENTK 60

RESULT 29
YHGB BACSU
ID YHGB BACSU STANDARD; PRT; 104 AA.
AC P38048;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein yhgB.
GN YHGB OR BSU10090.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=982040224; PubMed=9579061;
RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
RA Wedler H., Venema G., Bron S.;
RT "The 172 kb prkA-addAB region from 83 degrees to 97 degrees of the
RT Bacillus subtilis chromosome contains several dysfunctional genes,
RT the glyB marker, many genes encoding transporter proteins, and the
RT ubiquitous hit gene."
RL Microbiology 144:859-875 (1998).
RV [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Barbero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier V., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,

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RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Yamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Toseato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RT Nature 390:249-256 (1997).
RL Nature 390:249-256 (1997).
RN [3]
RP SEQUENCE OF 1-67 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Popham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the Bacillus
RT subtilis pbpF gene, which codes for a putative class A
RT high-molecular-weight penicillin-binding protein."
RT J. Bacteriol. 175:4870-4876 (1993).
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CC
DR EMBL; Y14083; CAA74515.1; -
DR EMBL; Y29109; CAB12849.1; -
DR EMBL; L10630; AAA71940.2; -
DR PIR; E69832; E69832.
DR Subtilist; BG10426; yhgB.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FD968 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 LMKSR 227
DB 25 LMKSR 30

RESULT 30
Y13K_NPVOP
ID Y13K_NPVOP STANDARD; PRT; 119 AA.
AC Q05122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 13.4 kDa protein in ubiquitin 3'region (Lambda 208).
OS Orygia pseudotsugata multicapsid polyhedrosis virus (OpMPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OX NCBI_TaxID=164623;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93286576; PubMed=8389803;
RA Russell R.L.Q., Rohrmann G.F.;
RT "Nucleotide sequence of the ubiquitin-39K gene region from the Orygia
RT pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."
RL J. Gen. Virol. 74:1191-1195 (1993).
CC

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CC -----
 CC EMBL; D13375; BAA02641.1; -;
 CC PIR; JQ2032; JQ2032.
 CC KW Hypothetical protein.
 CC SQ SEQUENCE 119 AA; 13415 MW; 8B35F990F5BD9678 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLRLV 88
 | | | | |
 Db 90 QLRLV 95

RESULT 31

ACPS VIBPA ID ACPS VIBPA STANDARD; PRT; 126 AA.
 AC Q87L3; 2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (SC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS OR VP2568.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RM2 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 RT distinct from that of *V. cholerae*.";
 RL Lancet 361:743-749 (2003).
 CC [-] FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC [-] CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3', 5'-bisphosphate + holo-[acyl-carrier protein].
 CC [-] COPACTOR: Magnesium (By similarity).
 CC [-] SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC [-] SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 CC family.

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CC EMBL; AP005082; BAC60831.1; -;
 CC HAMAP; MF 00101; -;
 CC DR InterPro; IPR008278; 4-PPT_transf.
 CC PFam; PF01648; ACPS; 1.
 CC KW Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 CC Complete proteome.
 CC METAL 9 9 MAGNESIUM (BY SIMILARITY).
 CC FT METAL 58 58 MAGNESIUM (BY SIMILARITY).
 CC SQ SEQUENCE 126 AA; 13645 MW; C565B0E2812C3A3C CRC64;

Query Match 2.1%; Score 6; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 EKALGR 149
 | | | | |
 Db 17 EKALGR 22

RESULT 32

CRBL MYCTU ID CRBL MYCTU STANDARD; PRT; 132 AA.
 AC P95089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein crCB homolog 1.
 GN CRBL OR RV3069 OR MT3153.1 OR MTCY22D7.12C OR MB3096.
 OS Mycobacterium tuberculosis, and
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773, 1765;
 RN [1]

RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam I.A., Ermolaeva M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
 RT "Whole-genome comparison of *Mycobacterium tuberculosis* clinical and
 RT laboratory strains.";
 RL J. Bacteriol. 184:5479-5490 (2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RC SPECIES=M.bovis; STRAIN=AF2122/97;
 RX MEDLINE=22709107; PubMed=12788972;
 RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
 RT "The complete genome sequence of *Mycobacterium bovis*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
 CC [-] SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC [-] SIMILARITY: Belongs to the crCB family.

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CC EMBL; Z83866; CAB06254.1; -;
 CC EMBL; AB007132; AAK47489.1; -;

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DR EMBL; BX248344; CAD96783.1; -.
DR PIR; F70650; F70650.
DR TIGR; MT3153.1; -.
DR Tuberculist; RV3069; -.
DR HAMAP; MF_00454; -.
DR InterPro; IPR003691; Camphor_Crb.
DR Pfam; PF02537; CRCB; 1.
KW Transmembrane; Complete proteome.
FT TRANSMEM 9 31 POTENTIAL.
FT TRANSMEM 35 57 POTENTIAL.
FT TRANSMEM 70 92 POTENTIAL.
FT TRANSMEM 102 124 POTENTIAL.
SQ SEQUENCE 132 AA; 14301 MW; C49B283379B0174E CRC64;

Query Match          2.1%; Score 6; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      276 GAFLVG 281
Db      48 GAFLVG 53
|||||

RESULT 33
YB47_SNNY3
AC P73795; STANDARD; PRT; 137 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein sll1147.
GN SLL1147.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A. PubMed=8905231;
RX MEDLINE=97061201;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nariu K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the MAPEG family.
-----
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DR EMBL; D90309; BRA17849.1; -.
DR PIR; S74888; S74888.
DR InterPro; IPR001129; MAPEG.
DR Pfam; PF01124; MAPEG; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 5 25 POTENTIAL.
FT TRANSMEM 79 99 POTENTIAL.
FT TRANSMEM 109 129 POTENTIAL.
SQ SEQUENCE 137 AA; 15414 MW; 9741232427529924 CRC64;

Query Match          2.1%; Score 6; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      82 WQLRQL 87

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Db      129 WQLRQL 134
|||||

RESULT 34
B701_HSV6G
AC P30024; STANDARD; PRT; 143 AA.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional regulatory protein B701.
OS Human herpesvirus (type 6 / strain GS) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92148942; PubMed=1310766;
RG Geng Y., Chandran B., Josephs S.F., Wood C.;
RT "Identification and characterization of a human herpesvirus 6 gene
RT segment that trans activates the human immunodeficiency virus type 1
RT promoter.";
RL J. Virol. 66:1564-1570(1992).
CC -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
CC ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
CC HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPA
CC SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPA, EITHER
CC DIRECTLY OR INDIRECTLY.
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-----
DR EMBL; M81789; -; NOT ANNOTATED_CDS.
DR PIR; A42186; WMBE6H.
KW Transcription regulation; Trans-acting factor; Activator.
SQ SEQUENCE 143 AA; 16385 MW; D0CE4D7C2422AAD8 CRC64;

Query Match          2.1%; Score 6; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      100 ISTVQE 105
Db      110 ISTVQE 115
|||||

RESULT 35
YB83_METJA
AC Q58878; STANDARD; PRT; 152 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein M31483.
GN M31483.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sutton G.G., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Bult C.J., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

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RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RL jannaschii".
 CC Science 273:1058-1073 (1996).
 CC -----
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 CC -----
 CC EMBL; U67589; AAB99498.1; --
 DR PIR; B64485; B64485.
 DR TIGR; MJ1483; --
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 7
 SQ SEQUENCE 152 AA; 17659 MW; 90227132448E8802 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 142 KNEKAL 147
 Db 120 KNEKAL 125
 |||||

RESULT 36
 YAU5 SCHPO STANDARD; PRT; 165 AA.
 ID YAU5 SCHPO STANDARD; PRT; 165 AA.
 AC Q09905;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adaptin complex small chain homolog C3OD11.05.
 GN SPAC30D11.05.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hanlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grynolprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Farnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.",
 RL Nature 415:871-880 (2002).
 CC -!- SIMILARITY: Belongs to the adaptor complexes small subunit
 CC family.
 CC -----
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 CC -----
 CC EMBL; Z67961; CAA91891.1; --
 DR PIR; T38594; S62563.
 DR GeneDB SPombe; SPAC30D11.05; --
 DR InterPro; IPR000804; Clat adaptor s.
 DR Pfam; PF01217; Clat adaptor s; 1.
 DR PROSITE; PS00989; CLAT ADAPTOR S; 1.
 KW Hypothetical protein; Coated pits.
 SQ SEQUENCE 165 AA; 18642 MW; 9EA796AD34C40FF3 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 133 SNTLSS 138
 Db 155 SNTLSS 160
 |||||

RESULT 37
 TN15 HUMAN STANDARD; PRT; 174 AA.
 ID TN15 HUMAN STANDARD; PRT; 174 AA.
 AC Q95150;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 15 (Vascular
 DE endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
 GN TNFSF15 OR VEGI OR TLI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RX MEDLINE=99091541; PubMed=9872942;
 RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
 RA Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
 RA Li L.-Y., Gentz R., Yu G.-L.;
 RT "VEGI, a novel cytokine of the tumor necrosis factor family, is an
 RT angiogenesis inhibitor that suppresses the growth of colon carcinomas
 RT in vivo.",
 RL FASEB J. 13:181-189 (1999).
 CC -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
 CC (in vitro).
 CC -!- SUBUNIT: Homotrimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
 CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
 CC spleen, prostate, small intestine and colon.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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CC EMBL; AF039390; AAD08783.1; -
CC HSP; P50591; 1D0G.
CC Genew; HGNC:11931; TNFSF15.
CC MIM; 604052; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005102; F: receptor binding; TAS.
CC GO; GO:0000074; P: regulation of cell cycle; TAS.
CC InterPro; IPR0006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00049; TNF_2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152
FT CARBOHYD 152 152
SQ SEQUENCE 174 AA; 20131 MW; CCH83BA7EE673B98 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 PFGAFL 279
Db 168 PFGAFL 173

RESULT 38
YE18_METJA STANDARD; PRT; 181 AA.
AC Q58813;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 15-MAR-2004 (Rel. 43; Last annotation update)
DE Hypothetical aldolase class II protein MJ1418.
GN MJ1418.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.P., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Frazer C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073 (1996).
CC -!- COFACTOR: Binds 1 zinc ion per molecule (Potential).
CC -!- SIMILARITY: Belongs to the aldolase class II family. Arab/fuca
CC subfamily.
CC
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CC
CC EMBL; U67582; AAB99428.1; -
CC PIR; A64477; A64477.
CC HSP; P11550; 1DZX.
CC TIGR; MJ1418; -
CC InterPro; IPR001303; Aldolase_II_N.
CC Pfam; PF00596; Aldolase_II; 1.
CC Hypothetical protein; Zinc; Complete proteome.
FT METAL 68 68 ZINC (BY SIMILARITY).
FT METAL 87 87 ZINC (BY SIMILARITY).
FT METAL 89 89 ZINC (BY SIMILARITY).
FT METAL 147 147 ZINC (BY SIMILARITY).
SQ SEQUENCE 181 AA; 20470 MW; E5F3BF1372214590 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 FLKEDD 62
Db 45 FLKEDD 50

RESULT 39
NLPC_HAEIN STANDARD; PRT; 183 AA.
AC P45296;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 10-OCT-2003 (Rel. 42; Last annotation update)
DE Probable lipoprotein nlpc homolog precursor.
GN NLPC OR H11652.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd."
RL Science 269:496-512 (1995).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Probable).
CC -!- SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA P60 FAMILY.
CC
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CC
CC EMBL; U32838; AAC23297.1; -
CC PIR; H64173; H64173.
CC MEROPS; C40.UFW; -
CC TIGR; H11652; -
CC InterPro; IPR000064; Peptidase_C40.
CC InterPro; IPR000437; Prok_lipoprot_S.
CC Pfam; PF00877; NLPC_P60; 1.

```


DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 183 PROBABLE LIPOPROTEIN NLPC HOMOLOG.
 FT LIPID 18 18 N-palmitoyl cysteine (Potential).
 FT LIPID 18 18 S-diacylglycerol cysteine (Potential).
 SQ SEQUENCE 183 AA; 20585 MW; 772B857F79452E38 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 LGRKIN 152
 Db 121 LGRKIN 126

RESULT 40
 UBC4_WHEAT
 ID UBC4_WHEAT STANDARD; PRT; 184 AA.
 AC P16577;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ubiquitin-conjugating enzyme E2-23 kDa (EC 6.3.2.19)
 DE (Ubiquitin-conjugating ligase) (Ubiquitin carrier protein).
 GN UBC4.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Augusta;
 RX MEDLINE=9009364; PubMed=2557633;
 RA Sullivan M.L., Vierstra R.D.;
 RT "A ubiquitin carrier protein from wheat germ is structurally and
 RT functionally similar to the yeast DNA repair enzyme encoded by
 RT RAD6.";
 RL J. Biol. Chem. 266:23878-23885(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Augusta;
 RX MEDLINE=92084684; PubMed=1660887;
 RA Sullivan M.L., Vierstra R.D.;
 RT "Cloning of a 16-kDa ubiquitin carrier protein from wheat and
 RT Arabidopsis thaliana. Identification of functional domains by in
 RT vitro mutagenesis.";
 RL J. Biol. Chem. 266:23878-23885(1991).
 RN [2]
 RP FUNCTION: Catalyzes the covalent attachment of ubiquitin to other
 CC proteins.
 CC -1- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
 CC diphosphate + protein N-ubiquityllysine.
 CC -1- PATHWAY: Ubiquitin conjugation; second step.
 CC -1- MISCELLANEOUS: A cysteine residue is required for ubiquitin-
 CC thiolester formation.
 CC -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
 CC
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 CC
 CC EMBL; M28059; AAA34309.1; -
 CC PIR; A34506; A34506.
 CC HSP; Q95044; 2B2C.
 CC InterPro; IPR000608; UBQ_conjugat.
 CC Pfam; PF001179; UQ_con; 1.
 CC ProDom; PD000461; UBQ_conjugat; 1.
 CC SMART; SM00212; UBCc; 1.

DR PROSITE; PS00183; UBIQUITIN_CONJUGAT 1; 1.
 DR PROSITE; PS00127; UBIQUITIN_CONJUGAT 2; 1.
 KW Ub1 conjugation pathway; Ligase; Multigene family.
 FT BINDING 85 85 UBIQUITIN.
 FT DOMAIN 141 176 ASP/GLU-RICH (ACIDIC).
 FT MUTAGEN 85 85 C->S: LOSS OF ACTIVITY.
 SQ SEQUENCE 184 AA; 21125 MW; AA479C4B42C893B7 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 SIYQGG 246
 Db 42 SIYQGG 47

RESULT 41
 RL9_DROME
 ID RL9_DROME STANDARD; PRT; 190 AA.
 AC P50882; O9VKL6; O9VKL7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 60S ribosomal protein L9.
 GN RPL9 OR M(2)32D OR CG6141.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S.
 RX MEDLINE=96262152; PubMed=8676882;
 RA Schmidt A., Hollmann M., Schaefer U.;
 RT "A newly identified Minute locus, M(2)32D, encodes the ribosomal
 RT protein L9 in Drosophila melanogaster.";
 RL Mol. Gen. Genet. 251:381-387(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dabson K., Doup L.E., Downes M., Dugan-Rocha S., Durkin J.A., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Hostin N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 FT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -1- SIMILARITY: Belongs to the L6P family of ribosomal proteins.
 CC -----
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 CC -----
 DR EMBL; X94613; CAA64319.1; -;
 DR EMBL; AE003630; AAF53048.2; -;
 DR PIR; JC6062; JG6062.
 DR FlyBase; FBgn0015756; RPL9.
 DR InterPro; IPR000702; Ribosomal L6.
 DR Pfam; PF00347; Ribosomal L6; 2_
 DR PROSITE; PS00700; RIBOSOMAL_L6_2; 1.
 KW Ribosomal protein.
 FT CONFLICT 37 S -> T (IN REF. 1).
 SQ SEQUENCE 190 AA; 21392 MW; 689B2520ACDA12D3 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 190;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 126 ITGTRG 131
 DB 27 ITGTRG 32
 RESULT 42
 COAE STRCO STANDARD; PRT; 200 AA.
 AC Q952K7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase).
 GN COAE OR SCO1996 OR SC7H2.10C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 ON NCBI_TaxID=1902;
 RX STRAIN=A3(2) / M145;
 RP SEQUENCE FROM N.A.
 RC STRAIN=21996410; PubMed=12000953;
 RX Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Reil S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RL coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- FUNCTION: Catalyzes the phosphorylation of the 3'-hydroxyl group
 CC of dephosphocoenzyme A to form coenzyme A (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + dephospho-CoA = ADP + CoA.
 CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; fifth (last) step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the coae family.
 CC -----
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 CC -----
 DR EMBL; AL939111; CAB52052.1; -;
 DR PIR; T35741; T35741.
 DR HAMAP; MF_00376; -; 1.
 DR InterPro; IPR001977; Depp_CoAkinase.
 DR Pfam; PF01121; CoaE; 1.
 DR ProDom; PD003329; Depp_CoAkinase; 1.
 DR TIGRFAMs; TIGR00152; TIGR00152; 1.
 DR PROSITE; PS01294; COAE; 1.
 DR Transferrase; Kinase; ATP-binding; Coenzyme A biosynthesis;
 KW Complete proteome.
 FT NP BIND 8 15 ATP (POTENTIAL).
 SQ SEQUENCE 200 AA; 21500 MW; FC2F5151EBEF33AE CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 112 PLVRR 117
 DB 89 PLVRR 94
 RESULT 43
 GLOB TOBAC STANDARD; PRT; 209 AA.
 AC Q034I6;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein GLOBOSA.
 GN GLO.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 ON NCBI_TaxID=4097;
 RX STRAIN=cv. SR1; TISSUE=Flower;
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93288002; PubMed=8099711;
 RX Hansen G., Estruch J.J., Sommer H., Spena A.;
 RT "NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of
 RL Antirrhinum majus: cDNA sequence and expression pattern.";
 RL Mol. Gen. Genet. 239:310-312(1993).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC THE FLOWER EXPRESSION IS RESTRICTED TO PETALS AND STAMENS.
 CC -1- MISCELLANEOUS: MUTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS

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CC      INTO SEALS AND STAMINA INTO CARPELS.
CC      -!- SIMILARITY: Contains 1 K-box dimerization domain.
CC      -!- SIMILARITY: Contains 1 MADS-box domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X67959; CAA48142.1; -.
CC      PIR: S35226; S35226.
CC      HSSP: P11746; 1MNM.
CC      TRANSFAC: T01779; -.
CC      InterPro: IPR002487; TF_Kbox.
CC      Pfam: PF01486; K-box; 1.
CC      PRINTS: PF00319; SRP-TF; 1.
CC      SMART: SM00404; MADSDOMAIN.
CC      PROSITE: PS00350; MADS_BOX_1; 1.
CC      PROSITE: PS50066; MADS_BOX_2; 1.
CC      Transcription regulation; DNA-binding; Activator; Nuclear protein;
CC      Developmental protein.
CC      DOMAIN 3 57 MADS-box.
CC      DOMAIN 91 163 K-BOX.
CC      SEQUENCE 209 AA; 24691 MW; 5661F9C1640E1A47 CRC64;
CC
CC      Query Match 2.1%; Score 6; DB 1; Length 209;
CC      Best Local Similarity 100.0%; Pred. No. 1.5e+02;
CC      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 82 WQLRQL 87
CC      DB 160 WQLRQL 165
CC
CC      RESULT 44
CC      CYC4_AZOVI
CC      ID -CYC4_AZOVI STANDARD; PRT; 210 AA.
CC      AC P43302;
CC      DT 01-NOV-1995 (Rel. 32, Created)
CC      DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC      DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC      DE Cytochrome C4 precursor.
CC      GN CYC4.
CC      OS Azotobacter vinelandii.
CC      OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC      OC Pseudomonadaceae; Azotobacter.
CC      OX NCBI_TaxID=354;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=CA;
CC      RX MEDLINE=95345104; PubMed=7619830;
CC      RA Ng T.C.N., Laheri A.N., Maier R.J.;
CC      RT "Cloning, sequencing, and mutagenesis of the cytochrome c4 gene from
CC      RT Azotobacter vinelandii: characterization of the mutant strain and a
CC      RT proposed new branch in the respiratory chain.";
CC      RL Biochim. Biophys. Acta 1230:119-129(1995).
CC      RN [2]
CC      RP SEQUENCE OF 21-210.
CC      RC STRAIN=ATCC 13705 / OPI;
CC      RX MEDLINE=84307416; PubMed=6089759;
CC      RA Ambler R.P., Daniel M., Mellis K., Stout C.D.;
CC      RT "The amino acid sequence of the dihaem cytochrome c4 from the
CC      RT bacterium Azotobacter vinelandii.";
CC      RL Biochem. J. 222:217-227(1984).
CC      CC -!- FUNCTION: DIHEME, HIGH POTENTIAL CYTOCHROME C BELIEVED TO BE AN
CC      CC INTERMEDIATE ELECTRON DONOR TO TERMINAL OXIDATION SYSTEMS.
CC      CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC      CC -!- PTM: Binds 2 heme groups per molecule.

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CC      -----
CC      EMBL: L37290; AAA87314.1; -.
CC      PIR: I39740; I39740.
CC      HSSP: Q52369; IETP.
CC      InterPro: IPR008169; Cyt_C_bact.
CC      InterPro: IPR003088; Cyt_C1.
CC      InterPro: IPR008168; Cyt_C1C.
CC      InterPro: IPR000345; CytC_heme_BS.
CC      Pfam: PF00034; cytochrome_C_1.
CC      PRINTS: PR00605; CYTOCHROME_C1.
CC      PRODOM: PD004020; Cyt_C_bact; 2.
CC      PROSITE: PS00190; CYTOCHROME_C; 2.
CC      KW Electron transport; Heme; Periplasmic; Signal.
CC      FT SIGNAL 1 20
CC      FT CHAIN 21 210 CYTOCHROME C4.
CC      FT BINDING 34 34 HEME 1 (COVALENT).
CC      FT BINDING 37 37 HEME 1 (COVALENT).
CC      FT METAL 38 38 IRON (HEME 1 AXIAL LIGAND).
CC      FT METAL 86 86 IRON (HEME 1 AXIAL LIGAND).
CC      FT BINDING 139 139 HEME 2 (COVALENT).
CC      FT BINDING 142 142 HEME 2 (COVALENT).
CC      FT METAL 143 143 IRON (HEME 2 AXIAL LIGAND).
CC      FT METAL 187 187 IRON (HEME 2 AXIAL LIGAND).
CC      SQ SEQUENCE 210 AA; 21687 MW; 4B09C4AA90D1FC74 CRC64;
CC
CC      Query Match 2.1%; Score 6; DB 1; Length 210;
CC      Best Local Similarity 100.0%; Pred. No. 1.5e+02;
CC      Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 42 LKQMQD 47
CC      DB 61 LKQMQD 66
CC
CC      RESULT 45
CC      RPOA_ASTLO
CC      ID RPOA_ASTLO STANDARD; PRT; 220 AA.
CC      AC P34778; P58144;
CC      DT 01-FEB-1994 (Rel. 28, Created)
CC      DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC      DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC      DE DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (PEP) (Plastid-
CC      DE encoded RNA polymerase alpha subunit) (RNA polymerase alpha subunit).
CC      GN RPOA.
CC      OS Astasia longa (Euglenophyceae alga).
CC      OC Chloroplast.
CC      OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
CC      OX NCBI_TaxID=3037;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=CCAP 1204-17a;
CC      RX MEDLINE=95163124; PubMed=7859309;
CC      RA Gockel G., Hachtel W., Baier S., Fliss C., Henke M.;
CC      RT "Genes for components of the chloroplast translational apparatus are
CC      RT conserved in the reduced 73-kb plastid DNA of the nonphotosynthetic
CC      RT euglenoid flagellate Astasia longa.";
CC      RL Curt. Genet. 26:256-262(1994).
CC      RN [2]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=CCAP 1204-17a;
CC      RX MEDLINE=21080522; PubMed=11212895;
CC      RA Gockel G., Hachtel W.;
CC      RT "Complete gene map of the plastid genome of the nonphotosynthetic
CC      RT euglenoid flagellate Astasia longa.";
CC      RL Protist 151:347-351(2000).

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RV RP IDENTIFICATION OF GENE.
RX MEDLINE=21851312; PubMed=11861918;
RA Shevelova E.V., Giordani N.V., Hallick R.B.;
RT "Identification and comparative analysis of the chloroplast
RT alpha-subunit gene of DNA-dependent RNA polymerase from seven Euglena
RT species.";
RL Nucleic Acids Res. 30:1247-1254 (2002).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA] (N).
CC -!- SUBUNIT: In chloroplasts the minimal PEP RNA polymerase is
CC composed of four subunits: alpha, beta, beta', and beta'' (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
CC -!- CAUTION: Ref.1 and Ref.2 sequences differ from that shown due to
CC erroneous gene model prediction.
CC -!- CAUTION: The C-terminal domain thought to be required for
CC interaction with some regulatory factors is missing from this
CC protein.
CC
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CC
CC EMBL; AJ294725; CAC24589.1; ALT_SEQ.
CC EMBL; AJ294725; CAC24588.1; ALT_SEQ.
CC FIR; S38600; S38600.
CC HAMAP; MF_00059; atypical; 1.
CC InterPro; IPR009025; RBP1-like RNAPo.
CC InterPro; IPR001700; RNA pol. bac. org.
CC Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
CC SEQUENCE 220 AA; 26287 MW; D221F70D995BB5AB CRC64;
CC
CC Query Match 2.1%; Score 6; DB 1; Length 220;
CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 194 BEIKEN 199
CC DB 84 BEIKEN 89
CC
CC RESULT 46
CC THY2_XENLA
CC ID THY2_XENLA STANDARD; PRT; 224 AA.
CC AC Q00643;
CC DT 01-JUL-1993 (Rel. 26, Created)
CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Thyroliberin precursor 2 (thyrotropin releasing hormone) (TRH).
CC OS Xenopus laevis (African clawed frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
CC OC Xenopodinae; Xenopus.
CC NCBI_TaxID=8355;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Brain;
CC RA Bulant M., Richter K., Kuchler K., Kreil G.;
CC RT "A cDNA from brain of Xenopus laevis coding for a new precursor of
CC RT thyrotropin-releasing hormone.";
CC RL FEBS Lett. 296:292-296 (1992).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: This precursor contains seven copies of

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thyroliberin.
CC -!- MISCELLANEOUS: There are at least two genes for TRH in Xenopus.
CC
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CC
CC EMBL; X64056; CAA45412.1; --
CC FIR; S20382; S20382.
CC InterPro; IPR008857; TRH.
CC Pfam; PF05438; TRH; 1.
CC Amidation; Hormone; Repeat; Signal;
CC Cleavage on pair of basic residues; Multigene family;
CC Pyroglutamate carboxylic acid.
CC SIGNAL 1 15 BY SIMILARITY.
CC CHAIN 16 224 PROTHYROLIBERIN 2.
CC PEPTIDE 75 77 THYROLIBERIN.
CC PEPTIDE 89 91 THYROLIBERIN.
CC PEPTIDE 105 107 THYROLIBERIN.
CC PEPTIDE 119 121 THYROLIBERIN.
CC PEPTIDE 151 153 THYROLIBERIN.
CC PEPTIDE 166 168 THYROLIBERIN.
CC PEPTIDE 191 193 THYROLIBERIN.
CC MOD RES 75 75 PYROLIDONE CARBOXYLIC ACID.
CC MOD RES 77 77 AMIDATION (G-78 PROVIDE AMIDE GROUP).
CC MOD RES 89 89 PYROLIDONE CARBOXYLIC ACID.
CC MOD RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
CC MOD RES 105 105 PYROLIDONE CARBOXYLIC ACID.
CC MOD RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
CC MOD RES 119 119 PYROLIDONE CARBOXYLIC ACID.
CC MOD RES 121 121 AMIDATION (G-122 PROVIDE AMIDE GROUP).
CC MOD RES 151 151 PYROLIDONE CARBOXYLIC ACID.
CC MOD RES 153 153 AMIDATION (G-154 PROVIDE AMIDE GROUP).
CC MOD RES 166 166 PYROLIDONE CARBOXYLIC ACID.
CC MOD RES 168 168 AMIDATION (G-169 PROVIDE AMIDE GROUP).
CC MOD RES 191 191 PYROLIDONE CARBOXYLIC ACID.
CC MOD RES 193 193 AMIDATION (G-194 PROVIDE AMIDE GROUP).
CC SEQUENCE 224 AA; 26148 MW; 5F65114D5169BF15 CRC64;
CC
CC Query Match 2.1%; Score 6; DB 1; Length 224;
CC Best Local Similarity 100.0%; Pred. No. 1.6e+02;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 191 RFQEEI 196
CC DB 80 RFQEEI 85
CC
CC RESULT 47
CC THY1_XENLA
CC ID THY1_XENLA STANDARD; PRT; 227 AA.
CC AC P01152;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 01-FEB-1991 (Rel. 17, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Thyroliberin precursor 1 (thyrotropin releasing hormone) (TRH).
CC OS Xenopus laevis (African clawed frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
CC OC Xenopodinae; Xenopus.
CC NCBI_TaxID=8355;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Skin;
CC RA Kuchler K., Richter K., Trnovsky J., Egger R., Kreil G.;
CC RT "Two precursors of thyrotropin-releasing hormone from skin of Xenopus
CC RT laevis. Each contains seven copies of the end product.";
CC J. Biol. Chem. 265:11731-11733 (1990).

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RN RP SEQUENCE OF 1-123 FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=84182535; PubMed=6425056;
 RA Richter K., Kawashima E., Egger R., Kreil G.;
 RT "Biosynthesis of thyrotropin releasing hormone in the skin of Xenopus
 RL laevis: partial sequence of the precursor deduced from cloned cDNA.";
 CC EMBL J. 3:617-621(1984).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: This precursor contains seven copies of
 CC thyroliberin.
 CC -1- MISCELLANEOUS: There are at least two genes for TRH in Xenopus.
 CC
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 CC
 CC EMBL; M34699; AAA49973.1; -;
 CC EMBL; M34698; AAA49974.1; -;
 CC EMBL; X00770; CAA25345.1; ALT_TERM.
 CC PIR; A37061; RHXL.T
 CC InterPro; IPR008857; TRH.
 CC Pfam; PF05438; TRH; 1.
 CC Annotation; Hormone; Repeat; Signal;
 CC Cleavage on pair of basic residues; Multigene family;
 CC Pyrolydione carboxylic acid.
 CC SIGNAL 1 15
 CC CHAIN 16 227 PROTHYROLIBERIN 1.
 CC FT PEPTIDE 16 227 THYROLIBERIN.
 CC FT PEPTIDE 75 227 THYROLIBERIN.
 CC FT PEPTIDE 89 91 THYROLIBERIN.
 CC FT PEPTIDE 107 109 THYROLIBERIN.
 CC FT PEPTIDE 121 123 THYROLIBERIN.
 CC FT PEPTIDE 153 155 THYROLIBERIN.
 CC FT PEPTIDE 168 170 THYROLIBERIN.
 CC FT PEPTIDE 193 195 THYROLIBERIN.
 CC FT MOD_RES 75 75 PYROLYDIONE CARBOXYLIC ACID.
 CC FT MOD_RES 77 77 AMIDATION (G-78 PROVIDE AMIDE GROUP).
 CC FT MOD_RES 89 89 PYROLYDIONE CARBOXYLIC ACID.
 CC FT MOD_RES 91 91 AMIDATION (G-92 PROVIDE AMIDE GROUP).
 CC FT MOD_RES 107 107 PYROLYDIONE CARBOXYLIC ACID.
 CC FT MOD_RES 109 109 AMIDATION (G-110 PROVIDE AMIDE GROUP).
 CC FT MOD_RES 121 121 PYROLYDIONE CARBOXYLIC ACID.
 CC FT MOD_RES 123 123 AMIDATION (G-124 PROVIDE AMIDE GROUP).
 CC FT MOD_RES 153 153 PYROLYDIONE CARBOXYLIC ACID.
 CC FT MOD_RES 155 155 AMIDATION (G-156 PROVIDE AMIDE GROUP).
 CC FT MOD_RES 168 168 PYROLYDIONE CARBOXYLIC ACID.
 CC FT MOD_RES 170 170 AMIDATION (G-171 PROVIDE AMIDE GROUP).
 CC FT MOD_RES 193 193 PYROLYDIONE CARBOXYLIC ACID.
 CC FT MOD_RES 195 195 AMIDATION (G-196 PROVIDE AMIDE GROUP).
 CC FT VARIANT 46 46 L -> S.
 CC FT VARIANT 70 70 M -> I.
 CC FT VARIANT 218 220 MISSING.
 CC SEQUENCE 227 AA; 26336 MW; 7DEC001E3154CD47 CRC64;
 Query Match 2.4%; Score 6; DB 1; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 191 RFQEEI 196
 Db 80 RFQEEI 85
 RESULT 48
 HIS9 THEME STANDARD; PRT; 233 AA.
 ID HIS9 THEME
 AC Q9WZL1
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Probable histidinol-phosphatase (EC 3.1.3.15) (HolPase).
 GN HISK OR TM0804.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA Steward A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RL genome sequence of Thermotoga maritima.";
 CC Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)O = L-histidinol
 CC + phosphate.
 CC -1- PATHWAY: Histidine biosynthesis; eighth step.
 CC -1- SIMILARITY: BELONGS TO THE PHP FAMILY OF HYDROLASE. HISK FAMILY.
 CC
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 CC
 CC EMBL; AE001748; AAD35886.1; -;
 CC PIR; E72330; E72330.
 CC TIGR; TM0804; -;
 CC InterPro; IPR004013; PHP_C.
 CC InterPro; IPR003141; PHP_N.
 CC Pfam; PF02811; PHP_C; 1.
 CC Pfam; PF02231; PHP_N; 1.
 CC SMART; SM00481; POLIITAC; 1.
 CC Histidine biosynthesis; Hydrolase; Complete proteome.
 CC SEQUENCE 233 AA; 27144 MW; E0CE3D245E0EDA30 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 142 KNEKAL 147
 Db 153 KNEKAL 158
 RESULT 49
 RGS1 HUMAN
 ID RGS1_HUMAN STANDARD; PRT; 235 AA.
 AC Q9NS28;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Regulator of G-protein signaling 18 (RGS18).
 GN RGS18 OR RGS13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Wan T., Yuan Z., He L., Cao X.;
 RT "A novel regulator of G-protein signaling.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Platelet;

RA Gagnon A.W., Murray D.L., Leadley R.J. Jr.;
RT "Cloning and characterization of a novel regulator of G-protein
RL signaling in human platelets";
RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
EX PubMed-11042171;
RA Park I.K., Klug C.A., Li K., Jerabek L., Li L., Nanamori M.,
RA Neubig R.R., Hood L., Weissman I.L., Clarke M.F.;
RT "Molecular cloning and characterization of a novel regulator of
RT G-protein signaling from mouse hematopoietic stem cells";
RL J. Biol. Chem. 276:915-923 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutherford Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(1)-ALPHA AND G(Q)-ALPHA
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in peripheral leukocytes, bone
CC marrow, spleen and fetal liver.
CC -!- SIMILARITY: Contains 1 RGS domain.
CC -----
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CC -----
CC EMBL; AF076642; AAF80227.1; -.
CC EMBL; AF268036; AAK58589.1; -.
CC EMBL; BC020632; AAK20632.1; -.
CC HSSP; P49799; IAGR.
CC Genew; HGNC:14261; RGS18.
CC MIM; 607192;
CC InterPro; IPR000342; Regl_Gpotein.
CC Pfam; PF00615; RGS; 1.
CC PRINTS; PR01301; RGSPTROTEIN.
CC ProDom; PD001580; Regl_Gpotein; 1.
CC SMART; SM00315; RGS; 1.
CC PROSITE; PS00132; RGS; 1.
KW Signal transduction inhibitor.
FT DOMAIN 86 202 RGS.
FT CONFLICT 226 227 DV -> ML (IN REF. 3).
SQ SEQUENCE 235 AA; 27582 MW; 973ABDE8C7DE3D5 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 SRSRGH 161
Db 63 SRSRGH 68
|||||
RESULT 50
UBLI YEAST STANDARD; PERT; 236 AA.
AC P35127;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase YUHI (EC 3.4.19.12) (Ubiquitin
DE thiolesterase).
DE GN YUHI OR YJR099W OR J1941.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Miller H.I., Henzel W.J., Ridgway J.B., Kuang W.-J., Chisholm V.,
RA Liu C.-C.;
RT "Cloning and expression of a yeast ubiquitin-protein cleaving activity
RT in Escherichia coli.";
RL Biotechnology 7:698-704 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Ramezani Rad M., Kirchthath L., Hollenberg C.P.;
RA Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: Ubiquitin-protein hydrolase is involved both in the
CC processing of ubiquitin precursors and of ubiquitinated proteins.
CC This enzyme is a thiol protease that recognize and hydrolyze
CC a peptide bond at the C-terminal glycine of ubiquitin.
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -!- SIMILARITY: Belongs to peptidase family C12.
CC -----
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CC -----
CC EMBL; Z49599; CAA89629.1; -.
CC PIR; S51332; S51332.
CC PDB; 1CMX; 27-JUL-99.
CC Geronline; 141932; -.
CC MEROPS; C12.002; -.
CC SGD; S0003860; YUHI.
CC GO; GO:0005737; C:cytoplasm; IC.
CC InterPro; IPR001578; Peptidase_C12.
CC Pfam; PF01088; Peptidase_C12; 1.
CC PRINTS; PR00707; UECTHYDLASE.
CC ProDom; PD30862; UCH_1; 1.
CC PROSITE; PS00140; UCH_1; 1.
KW Ubiquitin conjugation pathway; Hydrolase; Thiol protease; 3D-structure.
FT ACT SITE 90 90
FT ACT SITE 166 166 BY SIMILARITY.
FT ACT SITE 181 181 BY SIMILARITY.
FT DOMAIN 43 60 UBIQUITIN BINDING 1 (POTENTIAL).
FT DOMAIN 175 183 UBIQUITIN BINDING 2 (POTENTIAL).
SQ SEQUENCE 236 AA; 26385 MW; D239FEE25798B395 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GGIFEL 250
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Db      175 GGIFEL 180
RESULT 51
F801 SCHMA
ID -F801 SCHMA          STANDARD;          PRT;    238 AA.
AC P16463;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Female specific 800 protein (FS800).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Platyhelminthes; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=89181810; PubMed=2927441;
RA Reis M.G., Kuhn J., Blanton R., Davis A.H.;
RT "Localization and pattern of expression of a female specific mRNA in
RT Schistosoma mansoni.";
RL Mol. Biochem. Parasitol. 32:113-119(1989).
CC -1- FUNCTION: FS800 is likely to have some function in the production
CC or maintenance of the schistosome egg.
CC -1- DEVELOPMENTAL STAGE: Highest level only in mature worms, i.e.,
CC during egg production.
CC -1- MISCELLANEOUS: The two F800 proteins are read from two
CC overlapping reading frames.
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-----
DR EMBL; J03999; AAA29883.1; -.
FT DOMAIN 42 45 POLY-ASN.
FT DOMAIN 72 77 POLY-ASP.
SQ SEQUENCE 238 AA; 27993 MW; FDFC8E9F4181B7F1 CRC64;
-----
Query Match 2.1%; Score 6; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 TRGRSN 134
Db 139 TRGRSN 144
-----
RESULT 52
PDXX SHEON
ID -PDXX SHEON          STANDARD;          PRT;    245 AA.
AC Q8E78;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pyridoxal phosphate biosynthetic protein pdxJ (PNP synthase).
GN PDXX OR S01351.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=MR-1.
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Teapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

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RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Mamathavan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., C.M.;
RA Feldblyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -1- FUNCTION: Catalyzes the condensation of 1-deoxy-D-xylulose-5-
CC phosphate (DXP) and 1-amino-3-(phosphohydroxy)propan-2-one to form
CC pyridoxine 5'-phosphate (PNP) [By similarity].
CC -1- PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and
CC pyridoxal phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the pdxJ family.
-----
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-----
DR EMBL; AB015579; AAN54416.1; -.
DR TIGR; S01351; -.
DR HAMAP; MF_00279; -.
DR InterPro; IPR004569; PdxJ.
DR Pfam; PF03740; PdxJ; 1.
DR TIGRFAMs; TIGR00559; pdxJ; 1.
KW Pyridoxine biosynthesis; Complete proteome.
SQ SEQUENCE 245 AA; 26559 MW; 9B6759082BA5AFF CRC64;
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Query Match 2.1%; Score 6; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 214 TSYDPDP 219
Db 22 TSYDPDP 27
-----
RESULT 53
THL1 ARATH
ID THL1 ARATH          STANDARD;          PRT;    247 AA.
AC Q9S720;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Unknown thylakoid lumen protein, chloroplast precursor.
GN ATIG76450 OR F14G6.5 OR F15M4.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

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RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:816-820 (2000).
 [2]
 RP SEQUENCE OF 81-89; 118-145; 166-181; 185-200 AND 218-236.
 RA Schubert M., Peterson U., Haas B., Funk C., Schroeder W.P.,
 RA Kieselbach T.;
 RT "The chloroplast lumen of Arabidopsis thaliana is a functionally
 RT important compartment";
 RL Submitted (AUG-2001) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 CC -!- CAUTION: Ref.1 sequences differ from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL; AC015450; AAG51945.1; ALT_SEQ.
 DR EMBL; AC012394; AAF16656.1; ALT_SEQ.
 KW Chloroplast; Thylakoid; Transit peptide.
 FT TRANSIT 1 26 CHLOROPLAST (POTENTIAL).
 FT TRANSIT 27 80 THYLAKOID.
 FT CHAIN 81 247 UNKNOWN THYLAKOID LUMEN PROTEIN.
 SQ SEQUENCE 247 AA; 27490 MW; FFD2B5627C7CE67 CRC64;

 Query Match 2.1%; Score 6; DB 1; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 179 KGFYII 184
 Db 184 KGFYII 189

 RESULT 54
 PSE3_HUMAN
 ID PSE3_HUMAN STANDARD; PRT; 254 AA.
 AC Q12920; O35563; P97373; Q13172; Q9BQD9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Proteasome activator complex subunit 3 (Proteasome activator 28-gamma
 DE subunit) (PA28gamma) (PA28g) (Activator of multicatalytic protease
 DE subunit 3) (11S regulator complex gamma subunit) (REG-gamma) (Ki
 DE nuclear autoantigen).
 GN PSME3.
 OS Homo sapiens (Human), and
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 10090;
 [1]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 EX MEDLINE=90183093; PubMed=1968796;
 RA Nikiido T., Shimada K., Shibata M., Hata M., Sakamoto M., Takasaki Y.,
 RA Sato C., Takahashi T., Nishida Y.;
 RT "Cloning and nucleotide sequence of cDNA for Ki antigen, a highly
 RT conserved nuclear protein detected with sera from patients with
 RT systemic lupus erythematosus";
 RL Clin. Exp. Immunol. 79:209-214 (1990).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP SPECIES=Human; TISSUE=B-cell, and Fetal brain;
 RX MEDLINE=95038831; PubMed=7951316;
 RA Albertsen H.M., Smith S.A., Mazoyer S., Fujimoto E., Stevens J.,

RA Williams B., Rodriguez P., Cropp C.S., Slijepcevic P., Carlson M.,
 RA Robertson M., Bradley P., Lawrence E., Harrington T., Sheng Z.M.,
 RA Hoopes R., Sternberg N., Brothman A., Callahan R., Ponder B.A.J.,
 RA White R.;
 RT "A physical map and candidate genes in the BRCA1 region on chromosome
 RT 17q12-21.";
 RL Nat. Genet. 7:472-479 (1994).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP SPECIES=Human; TISSUE=lung, Ovary, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [4]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=97364691; PubMed=9218537;
 RA Kandil E., Kohda K., Ishibashi T., Tanaka K., Kasahara M.;
 RT "PA28 subunits of the mouse proteasome: primary structures and
 RT chromosomal localization of the genes";
 RL Immunogenetics 46:337-344 (1997).
 [5]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Mouse; STRAIN=B10.BR;
 RX MEDLINE=97306277; PubMed=9162094;
 RA Jiang H., Monaco J.J.;
 RT "Sequence and expression of mouse proteasome activator PA28 and the
 RT related autoantigen Ki";
 RL Immunogenetics 46:93-98 (1997).
 [6]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Mouse; STRAIN=129/SvJ;
 RX MEDLINE=98250122; PubMed=9590240;
 RA Kohda K., Ishibashi T., Shimbara N., Tanaka K., Matsuda Y.,
 RA Kasahara M.;
 RT "Characterization of the mouse PA28 activator complex gene family:
 RT complete organizations of the three member genes and a physical map of
 RT the approximately 150-Kb region containing the alpha- and beta-subunit
 RT genes";
 RL J. Immunol. 160:4923-4935 (1998).
 [7]
 RN SEQUENCE OF 82-135 FROM N.A.
 RP SPECIES=Human; TISSUE=Ovary;
 RX MEDLINE=95025896; PubMed=7545954;
 RA Miki Y., Swensen J., Shattuck-Eidens D., Futreal P.A., Hershman K.,
 RA Tavtigian S., Liu Q., Cochran C., Bennett L.M., Ding W.;
 RT "A strong candidate for the breast and ovarian cancer susceptibility
 RT gene BRCA1";
 RL Science 266:66-71 (1994).
 CC -!- FUNCTION: Implicated in immunoproteasome assembly and required for
 CC efficient antigen processing. The PA28 activator complex enhances
 CC the generation of class I binding peptides by altering the
 CC cleavage pattern of the proteasome.
 CC -!- SUBUNIT: Homohexamers.
 CC -!- ALTERNATIVE PRODUCTS:


```
CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=1;
CC CC IsoId=Q12920-1; Sequence=Displayed;
CC CC Name=2;
CC CC IsoId=Q12920-2; Sequence=VSP_004516;
CC CC Note=Has been shown to exist only in human so far;
CC CC DISEASE: SERA FROM PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS
CC CC OFTEN CONTAIN ANTIBODIES THAT REACT WITH THE KI ANTIGEN.
CC CC -1- SIMILARITY: BELONGS TO THE PA28 FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; U11292; AAB60335.1; -
CC CC EMBL; BC008020; AAH08020.1; -
CC CC EMBL; BC001423; AAH01423.1; -
CC CC EMBL; BC002684; AAH02684.1; -
CC CC EMBL; D87911; BAA22041.1; -
CC CC EMBL; U60330; AAC53297.1; -
CC CC EMBL; AB007139; BAA28838.1; -
CC CC EMBL; U25756; AAA93227.1; -
CC CC PIR; I38702; A60537.
CC CC HSP; Q06323; IAVO.
CC CC Genew; HGNC:9570; PSME3.
CC CC GK; Q12920; -
CC CC MTM; G05129; -
CC CC MGD; MGI:1096366; Psme3.
CC CC GO; GO:0005837; C:26S proteasome; TAS.
CC CC InterPro; IPR003185; PA28_alpha.
CC CC InterPro; IPR003186; PA28_beta.
CC CC Pfam; PF02251; PA28_alpha.1.
CC CC Pfam; PF02252; PA28_beta.1.
CC CC Proteasome; Alternative splicing; Systemic lupus erythematosus.
CC CC VARSLIC 135 135
CC CC T -> TP5GKPHICFDLQ (in isoform 2).
CC CC /Ftda=VSP_004516.
FT FT CONFLICT 2 2 A -> L (IN REF. 5).
FT FT CONFLICT 9 9 Q -> L (IN REF. 5).
FT FT CONFLICT 23 23 T -> S (IN REF. 5).
FT FT CONFLICT 25 25 E -> K (IN REF. 2).
FT FT CONFLICT 94 94 E -> K (IN REF. 7).
FT FT CONFLICT 117 117 D -> G (IN REF. 5).
FT FT CONFLICT 172 172 A -> P (IN REF. 5).
FT FT CONFLICT 188 188 K -> G (IN REF. 5).
FT FT SEQUENCE 254 AA; 29506 MW; 116FAB47D60A26C0 CRC64;
CC CC
CC CC Query Match 2.1%; Score 6; DB 1; Length 254;
CC CC Best Local Similarity 100.0%; Pred. No. 1.8e+02;
CC CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC CC
CC CC QY 217 PDPILL 222
CC CC DB 67 PDPILL 72
CC CC
CC CC RESULT 55
CC CC OXAL_BACHD
CC CC ID_OXAL_BACHD STANDARD; PRT; 257 AA.
CC CC AC Q9RCAS5;
CC CC DT 15-MAR-2004 (Rel. 43, Created)
CC CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC CC DE Membrane protein oxa1 precursor.
CC CC GN OXA1 OR BH4064.
CC CC OS Bacillus halodurans.
CC CC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC CC OX NCBI_TaxID=86665;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC
CC CC STRAIN=C-125 / JCM 9153;
CC CC MEDLINE=99356711; PubMed=10427704;
CC CC Takami H., Masui N., Nakasone K., Horikoshi K.;
CC CC "replication origin region of the chromosome of alkaliphilic Bacillus
CC CC halodurans C-125.";
CC CC RN Biosci. Biotechnol. Biochem. 63:1134-1137(1999).
CC CC [2]
CC CC RP SEQUENCE FROM N.A.
CC CC STRAIN=C-125 / JCM 9153;
CC CC MEDLINE=20512582; PubMed=11058132;
CC CC Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
CC CC Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
CC CC Horikoshi K.;
CC CC "Complete genome sequence of the alkaliphilic bacterium Bacillus
CC CC halodurans and genomic sequence comparison with Bacillus subtilis.";
CC CC RN Nucleic Acids Res. 28:4317-4331(2000).
CC CC RT halodurans C-125.";
CC CC -1- FUNCTION: Required for the insertion of integral membrane proteins
CC CC into the membrane. May also be involved in protein secretion
CC CC processes (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC CC -1- SIMILARITY: Belongs to the OXA1/oxaA family. Subfamily 2.
CC CC -----
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CC CC -----
CC CC EMBL; AB013492; BAA82682.1; -
CC CC EMBL; AP001520; BAB07783.1; -
CC CC PIR; H84157; H84157.
CC CC HAMAP; MF_01811; 1.
CC CC InterPro; IPR001708; 60kDa_innermemb.
CC CC InterPro; IPR000437; Prok_lipoprot_S.
CC CC Pfam; PF02096; 60KD_IMP; 1.
CC CC PRINTS; PR00701; 60KDINNERMP.
CC CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC CC Transmembrane; Lipoprotein; Signal; Palmitate; Complete proteome.
CC CC SIGNAL 1 20 POTENTIAL.
CC CC CHAIN 21 257 MEMBRANE PROTEIN OXAA 1.
CC CC TRANSMEM 57 79 POTENTIAL.
CC CC TRANSMEM 125 147 POTENTIAL.
CC CC TRANSMEM 160 182 POTENTIAL.
CC CC TRANSMEM 202 224 POTENTIAL.
CC CC LIPID 21 21 N-palmitoyl cysteine (Potential).
CC CC LIPID 21 21 S-diacylglycerol cysteine (Potential).
CC CC SEQUENCE 257 AA; 29223 MW; 223AF5D688F161FD CRC64;
CC CC
CC CC Query Match 2.1%; Score 6; DB 1; Length 257;
CC CC Best Local Similarity 100.0%; Pred. No. 1.8e+02;
CC CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC CC
CC CC QY 217 PDPILL 222
CC CC DB 168 PDPILL 173
CC CC
CC CC RESULT 56
CC CC FLGG_BUCBP
CC CC ID_FLGG_BUCBP STANDARD; PRT; 260 AA.
CC CC AC Q89AH7;
CC CC DT 15-MAR-2004 (Rel. 43, Created)
CC CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC CC DE Flagellar basal-body rod protein flgg (Distal rod protein).
CC CC GN FLGG OR BBP13.
CC CC OS Buchnera aphidicola (subsp. Baizongia pistaciae).
CC CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC CC OC Enterobacteriaceae; Buchnera.
CC CC OX NCBI_TaxID=135842;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
RX MEDLINE=22426901; PubMed=12522265;
RA Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J., A.,
RA Tananes J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.,
RT "Reductive genome evolution in Buchnera aphidicola.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC -!- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
CC MOUNTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBUNITS OF
CC FLGG IN THE DISTAL PORTION, AND FLGB, FLGC AND FLGF ARE THOUGHT TO
CC BUILD UP THE PROXIMAL PORTION OF THE ROD WITH ABOUT 6 SUBUNITS
CC EACH (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the flagella basal body rod proteins
CC family.
CC
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CC
DR EMBL; AB014017; AAC27035.1; -.
DR InterPro; IPR001444; Flag_bb_rod.
DR Pfam; PF00460; flg_bb_rod; 1.
DR PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
KW Flagellum; Complete proteome.
SQ SEQUENCE 260 AA; 28215 MW; 0B9E1146CAD4690B CRC64;

Query Match 2.1%; Score 6; DB 1; Length 260;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SEETIS 101
Db 57 SEETIS 62

RESULT 57
RL1_HSV2H
ID RL1_HSV2H STANDARD; PRT; 261 AA.
AC P28283;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Neurovirulence factor (ICP34.5).
GN RL1.
OS Herpes simplex virus (type 2 / strain H52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
ON NCBI_TaxID=10315;
RX MEDLINE=92113549; PubMed=1662697;
RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
RT "Comparative sequence analysis of the long repeat regions and
RT adjoining parts of the long unique regions in the genomes of herpes
RT simplex viruses types 1 and 2.";
RL J. Gen. Virol. 72:3057-3075(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22113549; PubMed=1662697;
RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
RT "Comparative sequence analysis of the long repeat regions and
RT adjoining parts of the long unique regions in the genomes of herpes
RT simplex viruses types 1 and 2.";
RN [2]
RP SEQUENCE FROM N.A.

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CC EMBL; D10471; BAA23428.1; -.
DR EMBL; Z86099; CAB06759.1; -.
DR EMBL; Z86099; CAB06706.1; -.
DR FIR; JQ1502; WMBEXE.
KW Repeat.
FT DOMAIN 3 12 2 X 5 AA TANDEM REPEATS OF R-R-R-G-P.
FT REPEAT 3 7
FT REPEAT 8 12 2 X 8 AA TANDEM REPEATS OF P-R-P-G-A-P-A-
FT DOMAIN 16 31 V.
FT REPEAT 16 23
FT REPEAT 24 31
SQ SEQUENCE 261 AA; 27908 MW; 4BBD13AF3D906D71 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 261;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 ERGPQR 121
Db 121 ERGPQR 126

RESULT 58
TNF5_AOTTR
ID TNF5_AOTTR STANDARD; PRT; 261 AA.
AC Q9BDM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE L) (CD154 protein).
GN TNFSF5 OR CD40LG OR CD40L.
OS Aotus trivirgatus (Night monkey) (Douroucoulis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as Ige
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
DR EMBL; AF344860; AAK37542.1; -.
DR HSP; P29965; ITALY.
GO; GO:0016021; C:integral to membrane; ISS.
GO; GO:0005174; F:CD40 receptor binding; ISS.
GO; GO:0042100; P:B-cell proliferation; ISS.
GO; GO:0006954; P:inflammatory response; ISS.
GO; GO:0007159; P:leukocyte cell adhesion; ISS.

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DR GO: GO:0030168; P:Platelet activation; ISS.
 DR InterPro; IPR003263; TNF 5.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF 1.
 DR PRINTS; PR01702; CD40LIGAND.
 DR ProDom; PD008600; TNF 5; 1.
 DR SMART; SM00207; TNF 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS00049; TNF 2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 261
 FT CHAIN 113 261
 FT CHAIN 113 261
 FT DOMAIN 1 22
 FT TRANSMEM 23 43
 FT DOMAIN 44 261
 FT SITE 112 113
 FT DISULFID 178 218
 FT CARBOHYD 240 240
 SQ SEQUENCE 261 AA; 29357 MW; 85E1588B507901B5 CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 GGIFEL 250
 Db 226 GGIFEL 231
 RESULT 59
 TNF5_BOVIN STANDARD; PRT; 261 AA.
 AC P51749;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-related activation protein) (TRAP) (T cell antigen GP39).
 GN TNFSF5 OR CD40LG OR CD40L.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96006582; PubMed=7590981;
 RA Mertens B.E.L.C.; Muraki M.; Gaidulis L.;
 RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand and tumor necrosis factor alpha."
 RL Immunogenetics 42:430-431(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
 CC -1- PM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
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 CC -----
 CC EMBL; Z48469; CA88363.1; -.
 CC PIR; S53090; S53090.
 CC HSP; P29965; 1ALY.
 CC GO: GO:0016021; C:integral to membrane; ISS.
 CC GO: GO:0005174; F:CD40 receptor binding; ISS.
 CC GO: GO:0042100; P:B-cell proliferation; ISS.
 CC GO: GO:0006954; P:inflammatory response; ISS.
 CC GO: GO:0007159; P:leukocyte cell adhesion; ISS.
 CC GO: GO:0030168; P:platelet activation; ISS.
 DR InterPro; IPR003263; TNF 5.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF_like.
 DR Pfam; PF00229; TNF 1.
 DR PRINTS; PR01702; CD40LIGAND.
 DR ProDom; PD008600; TNF 5; 1.
 DR SMART; SM00207; TNF 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS00049; TNF 2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 261
 FT CHAIN 113 261
 FT CHAIN 113 261
 FT DOMAIN 1 22
 FT TRANSMEM 23 46
 FT DOMAIN 47 261
 FT SITE 112 113
 FT DISULFID 178 218
 FT CARBOHYD 240 240
 SQ SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787FD CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 180 GFYIY 185
 Db 167 GFYIY 172
 RESULT 60
 TNF5_CALJA STANDARD; PRT; 261 AA.
 AC Q9BDN3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).
 GN TNFSF5 OR CD40LG OR CD40L.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OC NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F.; Bostik P.; Mayne A.E.; King C.L.; Genain C.P.; Weiss W.R.; Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IGE

```

CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; AF344844; AAK37603.1; -.
CC HSP; P29965; IALY.
CC GO; GO:0016021; C: integral to membrane; ISS.
CC GO; GO:0005174; F: CD40 receptor binding; ISS.
CC GO; GO:0042100; P: B-cell proliferation; ISS.
CC GO; GO:0006954; P: inflammatory response; ISS.
CC GO; GO:0007159; P: leukocyte cell adhesion; ISS.
CC GO; GO:0030169; P: platelet activation; ISS.
CC InterPro; IPR003263; TNF 5.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01702; CD40LIGAND.
CC ProDom; PD008600; TNF 5; 1.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS50049; TNF 2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT CHAIN 113 261
FT DOMAIN 1 22
FT TRANSMEM 23 43
FT CHAIN 44 261
FT SITE 112 113
FT DISULFID 178 218
FT CARBOHYD 240 240
FT SEQUENCE 261 AA; 29360 MW; 10CA58BD923754EB CRC64;
Query Match 2.1%; Score 6; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 GGIFEL 250
DB 226 GGIFEL 231
RESULT 61
XNLA CLOSA
AC P17137;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN XNLA.
OS Clostridium saccharobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=169679;

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RN SEQUENCE FROM N.A.
RP STRAIN=P262;
RX MEDLINE=90245673; PubMed=2336398;
RA Zappe H., Jones W.A., Woods D.R.;
RT "Nucleotide sequence of a Clostridium acetobutylicum P262 xylanase
RT gene (xynB).";
RL Nucleic Acids Res. 18:2179-2179(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -!- CAUTION: Was originally thought to originate from
CC C.acetobutylicum.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M31726; AAA23287.1; -.
CC HSP; P36217; LXVO.
CC InterPro; IPR008985; ConA like lec gl.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL HYDROL F11 1; 1.
CC PROSITE; PS00777; GLYCOSYL HYDROL F11 2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 261
FT ACT SITE 152 152
FT ACT SITE 242 242
FT SEQUENCE 261 AA; 29032 MW; 339C3616F6FD14AE CRC64;
Query Match 2.1%; Score 6; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 VIFTVL 25
DB 6 VIFTVL 11
RESULT 62
CTE2 HUMAN
ID CTE2 HUMAN STANDARD; PRT; 262 AA.
AC Q8N6M3; Q9H3V1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein C20orf142 precursor.
GN C20ORF142.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blake S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

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RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharalain M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sultson J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871 (2001).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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 CC -----
 CC EMBL; AL117382; CAC04189.1; ALT_INIT.
 CC EMBL; BC029662; AAH29662.1;
 CC Genew; HGNC:16135; C20orf142.
 KW Signal; Transmembrane.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 262 PROTEIN C20ORF142.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 146 166 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 FT TRANSMEM 262 262 AA; 29855 MW; 3822E7CFB6CDEB CRC64;
 SQ SEQUENCE 262 AA; 29855 MW; 3822E7CFB6CDEB CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 SGHSFL 164

Db 153 SGHSFL 158

RESULT 63

CITE_MOUSE
 ID CITE_MOUSE STANDARD; PRT; 262 AA.
 AC P59266;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein C20orf142 homolog precursor.
 GN C20ORF142.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta, Cerebellum, and Vein;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirimi L.M., Kanapin A., Matsuda H.A., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagahima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyawah-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- CAUTION: Ref.1 (BAC29663) sequence differs from that shown due to
 CC a frameshift in position 192.
 CC -----
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 CC -----
 CC EMBL; AK036997; BAC29663.1; ALT_FRAME.
 CC EMBL; AK040900; BAC30737.1; -.
 CC EMBL; AK043244; BAC31503.1; -.
 CC MGD; MGI:2444508; D930001I22Rik.
 KW Signal; Transmembrane.
 FT SIGNAL 1 39 POTENTIAL.
 FT CHAIN 40 262 PROTEIN C20ORF142 HOMOLOG.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 146 166 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 FT TRANSMEM 262 262
 FT CONFLICT 169 169 E -> Q (IN REF. 1; BAC29663).
 FT CONFLICT 245 245 G -> P (IN REF. 1; BAC29663).

SQ SEQUENCE 262 AA; 30016 MW; D28B971C521953BC CRC64;
 Query Match 2.1%; Score 6; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 SGHSFL 164
 |||||
 Db 153 SGHSFL 158

RESULT 64
 YA23 METJA STANDARD; PRT; 262 AA.
 AC Q58429;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Hypothetical ABC transporter ATP-binding protein MJ1023.
 GN MJ1023.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RT Science 273:1058-1073 (1996).
 RL Science 273:1058-1073 (1996).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 CC -----
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 CC -----
 CC EMBL; U67545; AA899027.1; -.
 DR F1R; F64427; F64427.
 DR TIGR; MJ1023; -.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00005; ABC tran_1
 DR ProDom; PD000006; ABC transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC TRANSPORTER 1; 1.
 DR PROSITE; PS00893; ABC TRANSPORTER 2; 1.
 KW Hypothetical protein; ATP-binding; (POTENTIAL).
 FT NP BIND 37 44 ATP (POTENTIAL).
 SQ SEQUENCE 262 AA; 30316 MW; B195338E6CED777 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 IFELKE 252
 |||||
 Db 166 IFELKE 171

RESULT 65

YK06 YEAST
 ID YK06 YEAST STANDARD; PRT; 267 AA.
 AC P36040;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29; Last sequence update)
 DT 01-OCT-1994 (Rel. 30; Last annotation update)
 DE Hypothetical 30.7 kDa protein in STB6-LOS1 intergenic region.
 GN YKL206C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pohl T.M., Pohl F.M.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SIMILARITY.
 RA Bork P.;
 RL Unpublished observations (AUG-1994).
 CC -1- SIMILARITY: SOME, TO MAMMALIAN DEOXYRIBONUCLEASE I.
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 CC -----
 CC EMBL; Z28206; CAAB2051.1; -.
 DR PIR; S38044; S38044.
 DR GerMOnline; 139960; -.
 DR SGD; S0001689; YKL206C.
 KW Hypothetical protein.
 SQ SEQUENCE 267 AA; 30739 MW; D635C3EBC2E37C11 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 164 LSNIHL 169
 |||||
 Db 152 LSNIHL 157

RESULT 66
 TNF5_CHICK
 ID TNF5_CHICK STANDARD; PRT; 272 AA.
 AC Q918D8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 15-MAR-2004 (Rel. 43; Last sequence update)
 DT 15-MAR-2004 (Rel. 43; Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
 DE L) (CD154 protein).
 GN TNF5 OR CD40LG OR CD40L.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Spleen;
 RA Tregaskes C.A., Young J.R., Burnside J.;
 RT "Cloning of a putative chicken CD40 ligand."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
 CC proliferation in the absence of co-stimulus as well as IGE
 CC production in the presence of IL-4. Involved in immunoglobulin
 CC class switching (By similarity).
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an

CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AJ243435; CAB95748.2; -;
 CC HSSP: P29965; IALY.
 CC GO: GO:0016021; C: integral to membrane; ISS.
 CC GO: GO:0005174; P: CD40 receptor binding; ISS.
 CC GO: GO:0042100; P: B-cell proliferation; ISS.
 CC GO: GO:0006984; P: inflammatory response; ISS.
 CC GO: GO:0007159; P: leukocyte cell adhesion; ISS.
 CC GO: GO:0030168; P: platelet activation; ISS.
 CC InterPro: IPR003263; TNF_5.
 CC InterPro: IPR006052; TNF_family.
 CC InterPro: IPR008983; TNF-like.
 CC InterPro: IPR003636; TNF_subf.
 CC Pfam: PF00229; TNF; 1.
 CC PRINTS: PR01702; CD40LIGAND.
 CC ProDom: PD008600; TNF_5; 1.
 CC ProDom: PD02012; TNF_subf; 1.
 CC SMART: SM00207; TNF_1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 CC CHAIN 1 272
 CC TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC MEMBER 5, MEMBRANE FORM
 CC TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
 CC SIGNAL-ANCHOR (POTENTIAL).
 CC (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC CLEAVAGE (BY SIMILARITY).
 CC POTENTIAL.
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;
 CC
 CC Query Match 2.1%; Score 6; DB 1; Length 272;
 CC Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 182 YYYISQ 187
 CC |||||
 CC Db 181 YYYISQ 186
 CC
 CC RESULT 67
 CC DEFC ARATH STANDARD; PRT; 273 AA.
 CC AC Q9FUZ2; O8LEH0; Q949U8; Q9LYJ4;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE Peptide deformylase, chloroplast precursor (EC 3.5.1.88) (PDF)
 CC DE (Polypeptide deformylase).
 CC GN PDF1B OR AT5G14560 OR T15NL150.
 CC OS Arabidopsis thaliana (Mouse-ear cress).
 CC OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
 CC OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 CC OX NCBI_TaxID=3702;
 CC RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20514156; PubMed=11060042;
 RA Giglione C., Serero A., Pierre M., Boisson B., Meimel T.;
 RT "Identification of eukaryotic peptide deformylases reveals
 RL universality of N-terminal protein processing mechanisms.";
 RN EMBL J. 19:5916-5929(2000).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=2016721; PubMed=11130714;
 RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asanizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
 RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
 RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Stromatt C.,
 RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,
 RA Parnell L., Shan R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
 RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
 RA Entian K.-D., Terry N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
 RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirkee W., Mooijman P., Klein Lankhorst R.,
 RA Weitzenecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
 RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.;
 RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 RL thaliana.";
 RN Nature 408:823-826(2000).
 CC [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.K., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjail M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinoraki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RL genome.";
 RN Science 302:842-846(2003).
 CC [4]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.A.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Removes the formyl group from the N-terminal Met of
 CC newly synthesized proteins (By similarity).
 CC -!- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)O = formate +
 CC methionyl peptide.
 CC -!- COFACTOR: Binds 1 iron(II) ion (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast (Potential).
 CC -!- SIMILARITY: Belongs to the polypeptide deformylase family.
 CC -----
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EMBL; AF250958; AAC33972.1; --
 HSP; P27251; 2DEF
 InterPro; IPR000181; Pep_deformylase.
 Pfam; PF01327; Pep_deformylase; 1.
 PRINTS; PR01576; PDEFORMLASE.
 ProDom; PD003844; Pep_deformylase; 1.
 TIGRFAMs; TIGR00079; Pept_deformyl; 1.
 Protein biosynthesis; Hydrolase; Iron; Chloroplast; Transit peptide.
 TRANSIT 1 ? 273 CHLOROPLAST (POTENTIAL).
 CHAIN ? 273 PEPTIDE DEFORMYLASE.
 FT METAL 177 177 IRON (BY SIMILARITY).
 FT ACT SITE 214 214 IRON (BY SIMILARITY).
 FT METAL 171 171 IRON (BY SIMILARITY).
 FT METAL 213 213 IRON (BY SIMILARITY).
 FT METAL 217 217 IRON (BY SIMILARITY).
 FT CONFLICT 48 48 T -> N (IN REF. 4).
 FT CONFLICT 205 205 R -> S (IN REF. 1).
 SQ SEQUENCE 273 AA; 30610 MW; 25CDA90ED6D9603E CRC64;

Query Match 2.1%; Score 6; DB 1; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 YPDPIL 221
 Db 86 YPDPIL 91

RESULT 68

DEFCLYCSES
 ID DEFCLYCSES STANDARD; PRT; 279 AA.
 AC Q9FV54;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Peptide deformylase, chloroplast precursor (EC 3.5.1.88) (PDF)
 DE (Polypeptide deformylase).
 GN Lycopersicon esculentum (Tomato).
 OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20514156; PubMed=11060042;
 RA Giglione C., Serero A., Pierre M., Boisson B., Meimel T.;
 RT "Identification of eukaryotic peptide deformylases reveals
 universality of N-terminal protein processing mechanisms.";
 RL EMBO J. 19:5916-5929(2000).
 CC -!- FUNCTION: Removes the formyl group from the N-terminal Met of
 newly synthesized proteins (By similarity).
 CC -!- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)O = formate +
 methionyl peptide.
 CC -!- COFACTOR: Binds 1 iron(II) ion (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast (Potential).
 CC -!- SIMILARITY: Belongs to the polypeptide deformylase family.
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CC EMBL; AF250958; AAC33972.1; --
 DR HSP; P27251; 2DEF
 DR InterPro; IPR000181; Pep_deformylase.
 DR Pfam; PF01327; Pep_deformylase; 1.
 DR PRINTS; PR01576; PDEFORMLASE.
 DR ProDom; PD003844; Pep_deformylase; 1.
 DR TIGRFAMs; TIGR00079; Pept_deformyl; 1.
 DR Protein biosynthesis; Hydrolase; Iron; Chloroplast; Transit peptide.
 FT TRANSIT 1 ? 279 CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 279 PEPTIDE DEFORMYLASE.
 FT METAL 177 177 IRON (BY SIMILARITY).
 FT ACT SITE 214 214 IRON (BY SIMILARITY).
 FT METAL 220 220 BY SIMILARITY.
 FT METAL 223 223 IRON (BY SIMILARITY).
 SQ SEQUENCE 279 AA; 31197 MW; 750F6408FDAC4233 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 YPDPIL 221
 Db 92 YPDPIL 97

RESULT 69

KC2C ARATH
 ID KC2C ARATH STANDARD; PRT; 282 AA.
 AC P40229;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Casein kinase II beta' chain (CK II).
 GN CK2 OR AT4G17640 OR DL485W.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94339478; PubMed=8061317;
 RA Collinge M.A., Walker J.C.;
 RT "Isolation of an Arabidopsis thaliana casein kinase II beta subunit
 by complementation in Saccharomyces cerevisiae.";
 RL Plant Mol. Biol. 25:649-658(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98121113; PubMed=9461215;
 RA Bevan M., Bancroft I., Bent E., Love K., Goodman H.M., Dean C.,
 RA Bergkamp R., Dirkse W., van Staveren M., Striekema W., Drost L.,
 RA Ridley P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,
 RA Wedler H., Wedler E., Wambutt R., Weitzengraber T., Pohl T., Terryn N.,
 RA Gielen J., Villarroel R., De Clercq R., van Montagu M., Lecharny A.,
 RA Aubourg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,
 RA Kotter P., Entian K.-D., Rieger M., Schaefer M., Funk B.,
 RA Mueller-Auer S., Silvey M., James R., Monfort A., Pons A.,
 RA Puigdomenech P., Douka A., Vouklatou E., Milioni D., Hatzopoulos P.,
 RA Piravandi E., Obermaier B., Hilbert H., Dueterhoeft A., Moores T.,
 RA Jones J.D.G., Eberhart T., Palme K., Benes V., Rechmann S., Ansorge W.,
 RA Cooke R., Berger C., Delsen M., Voet M., Volckaert G., Mewes H.-W.,
 RA Klosterman S., Schueller C., Chaltatzis N.,
 RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
 Arabidopsis thaliana".
 RL Nature 391:485-488(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Dueterhoeft A., Striekema W., Entian K.-D., Terryn N.,

RA Harris B., Ansoerg W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Ransperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirks W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Felbausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Feilner R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedori F., Cooke R., Berger C., Monfort A., Casasuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Baques M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Tradeih J.,
RA Steneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney J., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Grant S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
CC -1- FUNCTION: Plays a complex role in regulating the basal catalytic
CC activity of the alpha subunit (By similarity).
CC -1- SUBUNIT: Tetramer composed of an alpha chain, an alpha', one beta
CC chain and one beta' chain.
CC -1- PTM: Phosphorylated by alpha chain (By similarity).
CC -1- SIMILARITY: Belongs to the casein kinase 2 beta chain family.
CC
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CC
CC EMBL; U03984; AAA3234.1; --
CC EMBL; Z97343; CAB10544.1; --
CC EMBL; AL161546; CAB78767.1; --
CC PIR; S47968; S47968.
CC InterPro; IPR000704; CAS_kinase_II.
CC Pfam; PF01214; CK_II_beta; 1.
CC PRINTS; PR00472; CAS_KINASEII.
CC ProDom; PD003829; CAS_kinase_II; 1.
CC PROSITE; PS01101; CK2_BETA; 1.
KW Transferase: Serine/threonine-protein kinase; Phosphorylation.
SQ SEQUENCE 282 AA; 31978 MW; 507EAB0A7415D1E6 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 ESRSG 160
Db 58 ESRSG 63

RESULT 70
DPHS SCHPO
ID DPHS SCHPO STANDARD; PRT; 283 AA.
AC 074838;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Probable diphthine synthase (EC 2.1.1.98) (Diphthamide biosynthesis
DE methyltransferase).
GN SPC576.14.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Spours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Honesby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer B., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Fumelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: Required for the methylation step in diphthamide
CC biosynthesis.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 2-(3-carboxy-3-
CC aminopropyl)-L-histidine = S-adenosyl-L-homocysteine + 2-[3-
CC carboxy-3-(methlammonio)propyl]-L-histidine.
CC -1- PATHWAY: Diphthamide biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the diphthine synthase family.
CC
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CC
CC EMBL; AL031798; CAA21193.1; --
CC PIR; T41424; T41424.
CC GeneDB SPombe; SPC576.14; --
CC InterPro; IPR000878; Cor/por_Metransf.
CC InterPro; IPR004551; Dphthm_Synthase.
CC

```
DR Pfam; PF00590; TP methylase; 1.
DR TIGRfam; TIGR00522; dph5; 1.
KW Transferrase; Methyltransferase.
SQ SEQUENCE 283 AA; 32044 MW; FF3300910CECIAD7 CRC64;

Query Match
Best Local Similarity 2.1%; Score 6; DB 1; Length 283;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 SLCVAV 33
DB 213 SLCVAV 218

RESULT 71
YNFH_ECOLI
ID YNFH_ECOLI STANDARD; PRT; 284 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Anaerobic dimethyl sulfoxide reductase chain ynfH (DMSO reductase
DE anchor subunit ynfH).
GN YNFH OR B1590.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayaishi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377 (1996).
CC -!- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON
CC VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS. THE C SUBUNIT ANCHORS
CC THE OTHER TWO SUBUNITS TO THE MEMBRANE AND STABILIZE THE CATALYTIC
CC SUBUNITS (By similarity).
CC -!- SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS: YNFF, THE
CC REDUCTASE; YNFG, AN ELECTRON TRANSFER PROTEIN, AND YNFH, A
CC MEMBRANE ANCHOR PROTEIN (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -!- SIMILARITY: Strong, to E.coli dmsC.
CC
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CC
CC EMBL; AF000254; AAC74662.1; -.
CC EMBL; D90801; BAA15314.1; ALT INIT.
CC EMBL; D90802; BAA15324.1; ALT_INIT.

DR PIR; H64914; H64914.
DR EcoGene; EG13846; ynfH.
DR InterPro; IPR007059; DmsC.
DR Pfam; PF04976; DmsC; 1.
KW Hypothetical protein; Oxidoreductase; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 9 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 10 30 POTENTIAL.
FT DOMAIN 31 45 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 46 66 POTENTIAL.
FT DOMAIN 67 86 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 87 107 POTENTIAL.
FT DOMAIN 108 115 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 116 136 POTENTIAL.
FT DOMAIN 137 148 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 POTENTIAL.
FT DOMAIN 170 180 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 181 201 POTENTIAL.
FT DOMAIN 202 222 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 223 243 POTENTIAL.
FT DOMAIN 244 250 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 251 271 POTENTIAL.
FT DOMAIN 272 284 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 284 AA; 30523 MW; 73F7D760FC4B1344 CRC64;

Query Match
Best Local Similarity 2.1%; Score 6; DB 1; Length 284;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 VIFTVL 25
DB 11 VIFTVL 16

RESULT 72
LPXC_CHLVC
ID LPXC_CHLVC STANDARD; PRT; 285 AA.
AC Q824Q4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-3-O-(3-hydroxypropyl) N-acetylglucosamine deacetylase
DE (EC 3.5.1.-) (UDP-3-O-acetyl-GlcNAc deacetylase).
GN LPXC OR CCA000088.
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147 (2003).
CC -!- FUNCTION: Involved in the biosynthesis of lipid A, a
CC phosphorylated glycolipid that anchors the lipopolysaccharide to
CC the outer membrane of the cell (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-3-O-(3-hydroxytetradecanoyl)-N-
CC acetylglucosamine + H(2)O = UDP-3-O-(3-hydroxytetradecanoyl)-
CC glucoseamine + acetate.
CC -!- PATHWAY: Lipid A biosynthesis; second step.
CC -!- SIMILARITY: Belongs to the lpxC family.
CC
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 CC -----

DR EMBL; AE016994; AAP04840.1; -
 DR TIGR; CCA00088; -
 DR HAMAP; MF 00388; -; 1.
 DR InterPro; IPR004463; LpxC.
 DR Pfam; PF03331; LpxC; 1.
 DR TIGRFAM8; TIGR00325; lpxC; 1.
 KW Hydrolase; Lipid A biosynthesis; Lipid synthesis; Complete proteome.
 SQ SEQUENCE 285 AA; 31421 MW; 300EC1D08DB403D9 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 ALGRKI 151
 |||||
 Db 274 ALGRKI 279

RESULT 73

YHCS_HAEIN STANDARD; PRT; 288 AA.
 AC P43011;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Putative HTH-type transcriptional regulator H11364 (ORF2).
 GN H11364.

OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=96186898; PubMed=8635745;
 RA Chandler M.S., Smith R.A.;
 RT "Characterization of the Haemophilus influenzae topA locus: DNA
 RL Gene 169:125-31(1996).
 [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.B., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RL Rd.";
 RC Science 269:496-512(1995).

CC -1- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
 CC -----

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 CC -----

DR EMBL; U20964; AAC43726.1; -
 DR PIR; U32816; AAC23011.1; -
 DR PIR; D64171; D64171.
 DR TIGR; H11364; -

DR InterPro; IPR000847; HTH_LysR.
 DR InterPro; IPR005119; LysR_subst.
 DR Pfam; PF00126; HTH_1; 1.
 DR Pfam; PF03466; LysR_substrate; 1.
 DR PROSITE; PS0931; HTH_LysR; 1.
 KW Hypothetical protein; Transcription regulation; DNA-binding;
 KW Complete proteome.
 FT DOMAIN 1 59 HTH_LysR-TYPE
 FT DNA_BIND 19 38 H-T-H MOTIF (POTENTIAL).
 FT CONFLICT 281 288 VTGISLNF -> RAFTFLSGGLGCLSEIWENHEDNI
 FT (IN REF. 1).
 SQ SEQUENCE 288 AA; 32422 MW; EEF3C22374352980 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 KQONIS 111
 |||||
 Db 24 KQONIS 29

RESULT 74

EGCI_LISIN STANDARD; PRT; 291 AA.
 AC O92A19;

DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Probable GTPase engC protein 1 (EC 3.6.1.-).
 GN ENGCI OR LIN1933.

OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaeser P., Frangeul L., Buchrieser C., Rueniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Chardit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkak G.,
 RA Madsen E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Norddick G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001)

CC -1- FUNCTION: Unusual circularly permuted GTPase that catalyzes rapid
 CC hydrolysis of GTP with a slow catalytic turnover (By similarity).
 CC -1- SUBUNIT: Monomer (Probable).
 CC -1- SIMILARITY: Contains 1 engC GTPase domain.

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 CC -----

DR EMBL; AL596170; CAC97163.1; -
 DR PIR; AC1674; AC1674.
 DR ListIat; LIN01933; -
 DR HAMAP; MF 01820; -; 1.
 DR InterPro; IPR004881; DUF258.
 DR Pfam; PF03193; DUF258; 1.
 DR TIGRFAM8; TIGR00157; TIGR00157; 1.
 DR PROSITE; PS09316; ENG_C GTPASE; 1.
 KW Hydrolase; GTP-binding; Complete proteome.

FT DOMAIN 72 219 ENGCGTPASE.
 FT NP_BIND 112 115 GTP (PROBABLE).
 FT NP_BIND 164 171 GTP (PROBABLE).
 FT NP_BIND 214 218 GTP (PROBABLE).
 FT SITE 245 258 KNUCKLE-LIKE CYSTEINE CLUSTER.
 SQ SEQUENCE 291 AA; 32741 MW; 2C489FBBFDD69A61 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 NISPLV 114
 Db 35 NISPLV 40

RESULT 75

EGCI_LISMO
 ID EGCI_LISMO STANDARD; PRT; 291 AA.
 AC Q8Y680;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Probable GTPase engC protein 1 (EC 3.6.1.-).
 GN EGCI OR LM01819.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
 CC -!- FUNCTION: Unusual circularly permuted GTPase that catalyzes rapid
 CC hydrolysis of GTP with a slow catalytic turnover (By similarity).
 CC -!- SUBUNIT: Monomer (Probable).
 CC -!- SIMILARITY: Contains 1 engC GTPase domain.
 CC
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 CC
 CC -----
 CC DR EMBL; AL591981; CAC99897.1; -.
 CC DR PIR; AC1302; AC1302.
 CC DR ListList; LM001819; -.
 CC DR HAMAP; MF_01820; -; 1.
 CC DR InterPro; IPR004881; DUF258.
 CC DR Pfam; PF03193; DUF258; 1.
 CC DR TIGRFAMs; TIGR00157; TIGR00157; 1.
 CC DR PROSITE; PS00936; ENGCGTPASE; 1.
 CC KW Hydrolase; GTP-binding; Complete proteome.
 FT DOMAIN 72 219 ENGCGTPASE.
 FT NP_BIND 112 115 GTP (PROBABLE).
 FT NP_BIND 164 171 GTP (PROBABLE).
 FT NP_BIND 214 218 GTP (PROBABLE).
 FT SITE 245 258 KNUCKLE-LIKE CYSTEINE CLUSTER.
 SQ SEQUENCE 291 AA; 32744 MW; 4C44B33EE7159B56 CRC64;

Query Match 2.1%; Score 6; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 NISPLV 114
 Db 35 NISPLV 40

Search completed: March 23, 2004, 09:22:44
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:21:00 ; Search time 22 seconds
(without alignments)

659.404 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVGGPSLGTCLIV.....NEHLMDHEASFFGAFLVG 281

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*

6: /cgn2_6/ptodata/2/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	100.0	281	1	US-08-670-354-2
2	281	100.0	281	3	US-08-584-031-1
3	281	100.0	281	3	US-08-780-496-1
4	281	100.0	281	3	US-08-883-086-10
5	281	100.0	281	3	US-09-320-424-2
6	281	100.0	281	4	US-09-333-593A-6
7	281	100.0	281	4	US-09-157-864-11
8	281	100.0	281	4	US-09-825-563-2
9	281	100.0	281	4	US-10-039-785-66
10	281	100.0	281	5	PCT-US96-10895-2
11	279	99.3	279	4	US-09-072-993C-3
12	187	66.5	253	3	US-09-320-424-11
13	187	66.5	253	4	US-09-825-563-11
14	187	66.5	256	3	US-09-320-424-13
15	187	66.5	256	4	US-09-825-563-13
16	174	61.9	177	3	US-09-105-343A-7
17	161	57.3	161	4	US-09-563-423-7
18	90	32.0	101	1	US-08-670-354-4
19	90	32.0	101	3	US-09-320-424-4
20	90	32.0	101	4	US-09-825-563-4
21	90	32.0	101	5	PCT-US96-10895-4
22	85	30.2	85	4	US-09-632-287A-12
23	24	8.5	59	4	US-09-621-976-6479
24	15	5.3	15	4	US-09-628-665-14
25	15	5.3	19	4	US-09-628-665-32
26	14	5.0	183	3	US-09-105-343A-8
27	14	5.0	291	1	US-08-670-354-6

28	14	5.0	291	3	US-09-320-424-6	Sequence 6, Appli
29	14	5.0	291	4	US-09-825-563-6	Sequence 6, Appli
30	14	5.0	291	5	PCT-US96-10895-6	Sequence 6, Appli
31	12	4.3	87	4	US-09-632-287A-13	Sequence 13, Appli
32	7	2.5	96	1	US-07-972-481-2	Sequence 2, Appli
33	7	2.5	172	4	US-09-134-001C-5649	Sequence 2, Appli
34	7	2.5	209	4	US-09-096-724B-8	Sequence 5649, Ap
35	7	2.5	209	4	US-09-096-724B-24	Sequence 24, Appli
36	7	2.5	274	4	US-09-489-039A-7595	Sequence 7595, Ap
37	7	2.5	429	4	US-09-198-452A-189	Sequence 189, App
38	7	2.5	554	4	US-08-909-125-6	Sequence 6, Appli
39	7	2.5	700	4	US-09-851-642-34	Sequence 34, Appli
40	7	2.5	2071	3	US-09-415-522-6	Sequence 6, Appli
41	6	2.1	6	4	US-09-628-665-13	Sequence 13, Appli
42	6	2.1	10	4	US-09-628-665-31	Sequence 31, Appli
43	6	2.1	24	4	US-09-612-402B-26	Sequence 26, Appli
44	6	2.1	28	4	US-09-030-619-50	Sequence 50, Appli
45	6	2.1	46	4	US-08-858-207A-268	Sequence 268, App
46	6	2.1	62	4	US-09-328-352-6548	Sequence 6548, Ap
47	6	2.1	78	4	US-09-107-532A-5502	Sequence 5502, Ap
48	6	2.1	83	4	US-09-543-681A-5440	Sequence 5440, Ap
49	6	2.1	87	4	US-09-328-352-5745	Sequence 5745, Ap
50	6	2.1	104	3	US-08-946-329A-99	Sequence 99, Appli
51	6	2.1	105	4	US-09-543-681A-8267	Sequence 8267, Ap
52	6	2.1	106	2	US-08-822-830B-4	Sequence 4, Appli
53	6	2.1	106	2	US-08-950-660-4	Sequence 4, Appli
54	6	2.1	106	4	US-09-157-452B-4	Sequence 4, Appli
55	6	2.1	106	4	US-08-454-899G-10	Sequence 10, Appli
56	6	2.1	106	5	PCT-US93-00030-4	Sequence 4, Appli
57	6	2.1	106	5	PCT-US93-00924-4	Sequence 4, Appli
58	6	2.1	114	4	US-09-621-976-5264	Sequence 5264, Ap
59	6	2.1	116	4	US-09-134-001C-5132	Sequence 5132, Ap
60	6	2.1	117	4	US-09-489-039A-9835	Sequence 9835, Ap
61	6	2.1	119	4	US-08-635-886C-248	Sequence 248, App
62	6	2.1	119	4	US-08-974-690C-248	Sequence 248, App
63	6	2.1	128	4	US-08-635-886C-240	Sequence 240, App
64	6	2.1	128	4	US-08-974-690C-240	Sequence 240, App
65	6	2.1	129	4	US-09-134-000C-3666	Sequence 3666, Ap
66	6	2.1	134	4	US-09-252-991A-18565	Sequence 18565, A
67	6	2.1	135	4	US-09-252-991A-22722	Sequence 22722, A
68	6	2.1	135	4	US-09-252-991A-27904	Sequence 27904, A
69	6	2.1	137	4	US-09-328-352-4265	Sequence 4265, Ap
70	6	2.1	138	4	US-09-134-001C-3776	Sequence 3776, Ap
71	6	2.1	140	4	US-09-134-000C-6375	Sequence 6375, Ap
72	6	2.1	144	4	US-09-593-887-8	Sequence 8, Appli
73	6	2.1	145	4	US-09-134-001C-3901	Sequence 3901, Ap
74	6	2.1	147	4	US-09-461-325-458	Sequence 458, App
75	6	2.1	147	4	US-10-012-542-458	Sequence 458, App
76	6	2.1	149	3	US-08-836-075A-34	Sequence 34, Appli
77	6	2.1	149	3	US-08-836-075A-34	Sequence 40, Appli
78	6	2.1	149	4	US-08-635-886C-244	Sequence 244, App
79	6	2.1	149	4	US-08-635-886C-247	Sequence 247, App
80	6	2.1	149	4	US-08-974-690C-244	Sequence 244, App
81	6	2.1	149	4	US-08-974-690C-247	Sequence 247, App
82	6	2.1	152	4	US-09-252-991A-31484	Sequence 31484, A
83	6	2.1	155	2	US-08-984-172-3	Sequence 3, Appli
84	6	2.1	161	4	US-09-134-001C-3996	Sequence 3996, Ap
85	6	2.1	166	4	US-09-615-192A-273	Sequence 273, App
86	6	2.1	174	4	US-09-131-237C-2	Sequence 2, Appli
87	6	2.1	184	2	US-08-533-298-4	Sequence 4, Appli
88	6	2.1	185	4	US-09-328-352-7577	Sequence 7577, Ap
89	6	2.1	192	1	US-08-086-428B-93	Sequence 93, Appli
90	6	2.1	192	2	US-08-468-570-93	Sequence 93, Appli
91	6	2.1	192	2	US-08-290-665A-93	Sequence 93, Appli
92	6	2.1	192	4	US-08-466-601A-93	Sequence 93, Appli
93	6	2.1	192	5	PCT-US95-10398-93	Sequence 93, Appli
94	6	2.1	193	4	US-08-635-886C-212	Sequence 212, App
95	6	2.1	193	4	US-08-974-690C-212	Sequence 212, App
96	6	2.1	194	4	US-08-311-731A-273	Sequence 273, App
97	6	2.1	202	4	US-09-134-000C-3978	Sequence 3978, Ap
98	6	2.1	204	4	US-09-252-991A-31049	Sequence 31049, A
99	6	2.1	211	4	US-09-543-681A-8111	Sequence 8111, Ap
100	6	2.1	214	2	US-08-984-172-1	Sequence 1, Appli

ALIGNMENTS

```

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 100.0%; Score 281; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60
QY 61 DDSYNDPNDDESMNFWQVQKWLRLVRLTSEETISTVQEKQKNISPLVRERGPQ 120
DB 61 DDSYNDPNDDESMNFWQVQKWLRLVRLTSEETISTVQEKQKNISPLVRERGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWSSRSGHFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWSSRSGHFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVVIYKYTSYDPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVVIYKYTSYDPDPILLMKSRNSCWSKDAEYGLY 240

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QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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RESULT 2

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US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

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Query Match 100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVYFTNKLKQMDKYSGIACFLKE 60
QY 61 DDSYNDPNDDESMNFWQVQKWLRLVRLTSEETISTVQEKQKNISPLVRERGPQ 120
DB 61 DDSYNDPNDDESMNFWQVQKWLRLVRLTSEETISTVQEKQKNISPLVRERGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWSSRSGHFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWSSRSGHFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVVIYKYTSYDPDPILLMKSRNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVVIYKYTSYDPDPILLMKSRNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

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RESULT 3

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US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: APO-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435

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QY 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNCSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 6

US-09-333-593A-6
; Sequence 6, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R. A.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSSEG
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-5008-2
; CURRENT APPLICATION NUMBER: US/09/333.593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-333-593A-6

Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNCSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L. 41,113
; REGISTRATION NUMBER: 6111.N CN1
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-11

Query Match 100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSDYDNDDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNCSKDAEYGLY 240
Db 181 FYIYSQTYFRFQBEIKENTKNDKQWQYIYKTSYTPDPILLMKSARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

US-09-825-563-2
; Sequence 2, Application US/09825563
; Patent No. 6521228

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; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-825-563-2

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||
Db      1  MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||

QY      61  DDSYDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||
Db      61  DDSYDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||

QY      121  RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG 180
      |||
Db      121  RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG 180
      |||

QY      181  FYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYDPDILLMKSNCSKDAEYGLY 240
      |||
Db      181  FYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYDPDILLMKSNCSKDAEYGLY 240
      |||

QY      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||
Db      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||

RESULT 9
US-10-039-785-66
; Sequence 66, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09

Query Match      100.0%; Score 281; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 5.6e-279;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||
Db      1  MAMMEVQGGPSLGGTCLVIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
      |||

QY      61  DDSYDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||
Db      61  DDSYDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
      |||

QY      121  RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG 180
      |||
Db      121  RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG 180
      |||

QY      181  FYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYDPDILLMKSNCSKDAEYGLY 240
      |||
Db      181  FYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYDPDILLMKSNCSKDAEYGLY 240
      |||

QY      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||
Db      241  SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
      |||

RESULT 10
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match
Best Local Similarity 100.0%; Score 281; DB 5; Length 281;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSYNDPNDDESMNSPCQVKQWLRLVTKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DSYNDPNDDESMNSPCQVKQWLRLVTKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNCSWCKDAEYGLYI 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNCSWCKDAEYGLYI 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6345388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3

Query Match
Best Local Similarity 99.3%; Score 279; DB 4; Length 279;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKEDD 62
Db 1 MMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKEDD 60

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QY 63 SYWDPNDESMNSPCQVKQWLRLVTKMLRTSEETISTVQEKQONISPLVRERGPO 122
Db 61 SYWDPNDESMNSPCQVKQWLRLVTKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 123 AAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFY 182
Db 121 AAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFY 180
QY 183 YIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNCSWCKDAEYGLYI 242
Db 181 YIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNCSWCKDAEYGLYI 240
QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match
Best Local Similarity 66.5%; Score 187; DB 3; Length 253;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRERGPOVAAHITGRGSRNTLSSPNSKNEKALGRKINSW 154
Db 67 TSEETISTVQEKQONISPLVRERGPOVAAHITGRGSRNTLSSPNSKNEKALGRKINSW 126
QY 155 ESSRSGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 214
Db 127 ESSRSGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYT 186
QY 215 SYDDPILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDDPILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
QY 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 13
US-09-825-563-11
; Sequence 11, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:

```

```

; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-11

Query Match      66.5%; Score 187; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.5e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRRGPGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
Db 67 TSEETISTVQEKQONISPLVRRGPGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 126
QY 155 ESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEEIKENTKNDKQWQYIYKYT 214
Db 127 ESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEEIKENTKNDKQWQYIYKYT 186
QY 215 SYDPDILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 187 SYDPDILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
QY 275 FGAFLVG 281
Db 247 FGAFLVG 253

RESULT 14
US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US/09/320,424
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-11

Query Match      66.5%; Score 187; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.6e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRRGPGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
Db 70 TSEETISTVQEKQONISPLVRRGPGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 129
QY 155 ESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEEIKENTKNDKQWQYIYKYT 214
Db 130 ESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEEIKENTKNDKQWQYIYKYT 189
QY 215 SYDPDILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPDILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249
QY 275 FGAFLVG 281
Db 250 FGAFLVG 256

RESULT 15
US-09-825-563-13
; Sequence 13, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US/09/825,563
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-825-563-13

Query Match      66.5%; Score 187; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.6e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRRGPGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
Db 70 TSEETISTVQEKQONISPLVRRGPGQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 129
QY 155 ESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEEIKENTKNDKQWQYIYKYT 214
Db 130 ESSRSGHSFSLNHLRNGELVIEHKGFYIYSQTYFRFOEEIKENTKNDKQWQYIYKYT 189
QY 215 SYDPDILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db 190 SYDPDILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249
QY 275 FGAFLVG 281
Db 250 FGAFLVG 256

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Db 250 FGAFLVG 256

RESULT 16

US-09-105-343A-7

; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105.343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-7

Query Match 61.9%; Score 174; DB 3; Length 177;
Best Local Similarity 100.0%; Pred. No. 7.7e-170; Indels 0; Gaps 0;
Matches 174; Conservative 0; Mismatches 0;

QY 105 EQQNISPLVRGQPVAAHITGTRSNLTSSPNSKNEKALGRKINSWESSRSGHSL 164
Db 1 EQQNISPLVRGQPVAAHITGTRSNLTSSPNSKNEKALGRKINSWESSRSGHSL 60
QY 165 SNLHRLNGELVTHEKGFYIYSQTFRQEEIKENTKDKQMVQIYKYTSYPPDILLMK 224
Db 61 SNLHRLNGELVTHEKGFYIYSQTFRQEEIKENTKDKQMVQIYKYTSYPPDILLMK 120
QY 225 SARNSCWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Db 121 SARNSCWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 174

RESULT 17

US-09-565-423-7

; Sequence 7, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-7

Query Match 57.3%; Score 161; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.3e-156; Indels 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 0;

QY 121 RVAAHITGTRSNLTSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
Db 1 RVAAHITGTRSNLTSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 60
QY 181 FYIYSQTFRQEEIKENTKDKQMVQIYKYTSYPPDILLMKSAKNSCWKDAEYGLY 240
Db 61 FYIYSQTFRQEEIKENTKDKQMVQIYKYTSYPPDILLMKSAKNSCWKDAEYGLY 120
QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 281
Db 121 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 161

RESULT 18

US-08-670-354-4
; Sequence 4, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822

```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 101 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-670-354-4

Query Match
Best Local Similarity 32.0%; Score 90; DB 1; Length 101;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDQKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDQKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90
Db 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90

RESULT 19
US-09-320-424-4
; Sequence 4, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
; US-09-320-424-4

Query Match
Best Local Similarity 32.0%; Score 90; DB 3; Length 101;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDQKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDQKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90
Db 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90

RESULT 20
US-09-825-563-4
; Sequence 4, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 101 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-670-354-4

Query Match
Best Local Similarity 32.0%; Score 90; DB 1; Length 101;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDQKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNKLQMDQKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90
Db 61 DDSYWDNDDESNMSPCWQVKWQLRLVRK 90

RESULT 21
PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
```



```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 101 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US96-10895-4

Query Match      32.0%; Score 90; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.1e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTCVLIVFTVLQSLCVAVTVVFTNELKOMQDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTCVLIVFTVLQSLCVAVTVVFTNELKOMQDKYSKSGIACFLKE 60

Qy 61 DDSDYDNDPDESMNSPCWQVQWQLRQLVRK 90
Db 61 DDSDYDNDPDESMNSPCWQVQWQLRQLVRK 90

RESULT 22
US-09-632-287A-12
; Sequence 12, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-287A-12

Query Match      30.2%; Score 85; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.4e-79;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 ERGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELV 175
Db 1 ERGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELV 60

Qy 176 IHEKGFYIYSQTYFRQEEIKENT 200
Db 61 IHEKGFYIYSQTYFRQEEIKENT 85

RESULT 23
US-09-621-976-6479
; Sequence 6479, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6479
; LENGTH: 59
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 27
; OTHER INFORMATION: Xaa = Glu,Gln
; NAME/KEY: UNSURE
; LOCATION: 34
; OTHER INFORMATION: Xaa = Glu,Val
; NAME/KEY: UNSURE
; LOCATION: 33,57
; OTHER INFORMATION: Xaa = Leu,Pro
; NAME/KEY: UNSURE
; LOCATION: 25,32
; OTHER INFORMATION: Xaa = Leu,Val
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-6479

Query Match      8.5%; Score 24; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTCVLCVLIIVFTV 24
Db 1 MAMMEVQGGPSLGTCVLCVLIIVFTV 24

RESULT 24
US-09-628-665-14
; Sequence 14, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-14

Query Match      5.3%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQEEIKENTKNDKQ 205
Db 1 RFQEEIKENTKNDKQ 15

RESULT 25
US-09-628-665-32
; Sequence 32, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628,665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771e1 Sequence
US-09-628-665-32

Query Match          5.3%; Score 15; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQEEIKENTKNDKQ 205
Db 3 RFQEEIKENTKNDKQ 17

RESULT 26
US-09-105-343A-8
; Sequence 8, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match          5.0%; Score 14; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 VQYIYKYTSYPDPI 220
Db 109 VQYIYKYTSYPDPI 122

RESULT 27
US-09-105-343A-8
; Sequence 6, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
```

```
US-08-670-354-6
; Sequence 6, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-6

Query Match          5.0%; Score 14; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 VQYIYKYTSYPDPI 220
Db 217 VQYIYKYTSYPDPI 230

RESULT 28
US-09-320-424-6
; Sequence 6, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
```

```

; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 291
; TYPE: PRT
; ORGANISM: murine
US-09-320-424-6

```

```

Query Match          5.0%; Score 14; DB 3; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 207 VOYIYKTSYDPPI 220
Db 217 VOYIYKTSYDPPI 230

```

```

RESULT 29
US-09-825-563-6
; Sequence 6, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 291
; TYPE: PRT
; ORGANISM: murine
US-09-825-563-6

```

```

Query Match          5.0%; Score 14; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 207 VOYIYKTSYDPPI 220
Db 217 VOYIYKTSYDPPI 230

```

```

RESULT 30
PCT-US96-10895-6
; Sequence 6, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

```

```

; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-6

```

```

Query Match          5.0%; Score 14; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 207 VOYIYKTSYDPPI 220
Db 217 VOYIYKTSYDPPI 230

```

```

RESULT 31
US-09-632-287A-13
; Sequence 13, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-09-632-287A-13

```

```

Query Match          5.0%; Score 12; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 183 YIYSQYFRFQE 194
Db 183 YIYSQYFRFQE 194

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Db 65 YIYSQYRFQE 76

RESULT 32
US-07-972-481-2
; Sequence 2, Application US/07972481
; Patent No. 5578453
; GENERAL INFORMATION:
; APPLICANT: MCDONALD, PETER J
; APPLICANT: JOHNSON, ALAN M
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS AND
; NUMBER OF INVENTION: USE OF RECOMBINANT ANTIGENS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE ROAD
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,481
; FILING DATE: 12-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: INTERNATIONAL PCT/AU91/00347
; FILING DATE: 09-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 446-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-972-481-2

Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEEIKE 198
Db 2 FQEEIKE 8

RESULT 33
US-09-134-001C-5649
; Sequence 5649, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; NUMBER OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5649

; LENGTH: 172
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5649

Query Match 2.5%; Score 7; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ASFFGAF 278
Db 105 ASFFGAF 111

RESULT 34
US-09-096-724B-8
; Sequence 8, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
; APPLICANT: McGarry, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: human
US-09-096-724B-8

Query Match 2.5%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 9 QEEIKEN 15

RESULT 35
US-09-096-724B-24
; Sequence 24, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
; APPLICANT: McGarry, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 209
; TYPE: PRT
; ORGANISM: human
US-09-096-724B-24

Query Match 2.5%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 9 QEEIKEN 15

Db 9 QEEIKEN 15

RESULT 36

US-09-489-039A-7595
; Sequence 7595, Application US/09489039A
; Patent No. 6610836

GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7595
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7595

Query Match 2.5%; Score 7; DB 4; Length 274;

Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 ISPLVRE 116
|||||||
Db 117 ISPLVRE 123

RESULT 37

US-09-198-452A-189
; Sequence 189, Application US/09198452A
; Patent No. 6559294

GENERAL INFORMATION:

; APPLICANT: Grifffais, R
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 189
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-189

Query Match 2.5%; Score 7; DB 4; Length 429;

Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSRGH 161
|||||||
Db 248 ESSRSRGH 254

RESULT 38

US-08-909-125-6
; Sequence 6, Application US/08909125
; Patent No. 6495737

GENERAL INFORMATION:

; APPLICANT: KLESSIG, DANIEL
; APPLICANT: GUO, AILAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMPROVING
; TITLE OF INVENTION: SALICYLIC ACID-INDEPENDENT SYSTEMIC ACQUIRED DISEASE RESISTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720

; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,125
; FILING DATE: 11-AUG-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,033
; FILING DATE: 12-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: JANET E. REED, PH.D.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-563-4100
; TELEFAX: 215-563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 554 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-909-125-6

Query Match 2.5%; Score 7; DB 4; Length 554;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 KALGRKI 151
|||||||
Db 477 KALGRKI 483

RESULT 39

US-09-831-642-34
; Sequence 34, Application US/09831642
; Patent No. 6635751

GENERAL INFORMATION:

; APPLICANT: HAZE, Kyosuke et al.
; TITLE OF INVENTION: ENDOPLASMIC RETICULUM STRESS TRANSCRIPTION FACTORS ATF6 AND CREB
; FILE REFERENCE: 1422-0474P
; CURRENT APPLICATION NUMBER: US/09/831,642
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-831-642-34

Query Match 2.5%; Score 7; DB 4; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TVLLQSL 29
|||||||
Db 263 TVLLQSL 269

RESULT 40
US-09-415-522-6
; Sequence 6, Application US/09415522A
; Patent No. 6291660
; GENERAL INFORMATION:
; APPLICANT: Gaffney, Thomas
; APPLICANT: Wendland, Juergen
; APPLICANT: Philippen, Peter
; TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And
; TITLE OF INVENTION: Development
; FILE REFERENCE: CGC2046
; CURRENT APPLICATION NUMBER: US/09/415.522A
; CURRENT FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2071
; TYPE: PRT
; ORGANISM: Ashbya gossypii
US-09-415-522-6

Query Match 2.5%; Score 7; DB 3; Length 2071;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 SSPNSKN 143
Db 48 SSPNSKN 54
|||||

RESULT 41
US-09-628-665-13
; Sequence 13, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831
; CURRENT APPLICATION NUMBER: US/09/628.665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-13

Query Match 2.1%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSQHS 162
Db 1 SRSQHS 6
|||||

RESULT 42
US-09-628-665-31
; Sequence 31, Application US/09628665
; Patent No. 6673771
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Kinoshita, Masahiko
; TITLE OF INVENTION: Methods of Inhibiting Osteoclast Activity
; FILE REFERENCE: UPN3831

; CURRENT APPLICATION NUMBER: US/09/628.665
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,094
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6673771el Sequence
US-09-628-665-31

Query Match 2.1%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 SRSQHS 162
Db 3 SRSQHS 8
|||||

RESULT 43
US-09-612-402B-26
; Sequence 26, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612.402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Chlamydia sp.
US-09-612-402B-26

Query Match 2.1%; Score 6; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 LSNLHL 169
Db 8 LSNLHL 13
|||||

RESULT 44
US-09-030-619-50
; Sequence 50, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 66081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO. 50
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-50

Query Match 2.1%; Score 6; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 RKWLR 94
Db 11 RKWLR 16

RESULT 45
US-08-858-207A-268
Sequence 268, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 268:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e

Query Match 2.1%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 FTNELK 43
Db 19 FTNELK 24

RESULT 46

US-09-328-352-6548
Sequence 6548, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6548
LENGTH: 62
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-6548

Query Match 2.1%; Score 6; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 IACFLK 59
Db 1 IACFLK 6

RESULT 47

US-09-107-532A-5502
Sequence 5502, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5502:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium


```

;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...78
; SEQUENCE DESCRIPTION: SEQ ID NO: 5502:
US-09-107-532A-5502
;
; Query Match      2.1%; Score 6; DB 4; Length 78;
; Best Local Similarity 100.0%; Pred. No. 1.6e+02;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      68 NDEESM 73
;         |||||
;         21 NDEESM 26
;
; RESULT 48
; US-09-543-681A-5440
; Sequence 5440, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5440
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-5440
;
; Query Match      2.1%; Score 6; DB 4; Length 83;
; Best Local Similarity 100.0%; Pred. No. 1.7e+02;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      86 QLVKRM 91
;         |||||
;         51 QLVKRM 56
;
; RESULT 49
; US-09-328-352-5745
; Sequence 5745, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5745
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-5745
;
; Query Match      2.1%; Score 6; DB 4; Length 87;
; Best Local Similarity 100.0%; Pred. No. 1.9e+02;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      19 IVIFTV 24
;         |||||
;         16 IVIFTV 21
;
; RESULT 50
; US-08-946-329A-99
; Sequence 99, Application US/08946329A
; Patent No. 6057091
; GENERAL INFORMATION:
; APPLICANT: Beachy, Philip A.
; APPLICANT: Porter, Jeffrey A.
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,329A
; FILING DATE: 07-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/061,323
; FILING DATE: 07-OCT-1996
; APPLICATION NUMBER: 08/729,743
; FILING DATE: 10-JUL-1996
; APPLICATION NUMBER: 08/567,357
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/349,498
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-946-329A-99
;
; Query Match      2.1%; Score 6; DB 3; Length 104;
; Best Local Similarity 100.0%; Pred. No. 2.1e+02;
; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      170 RNGLV 175
;         |||||
;         44 RNGLV 49
;
; RESULT 51
; US-09-543-681A-8267
; Sequence 8267, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8267
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Proteus mirabilis

```

US-09-543-681A-8267

Query Match 2.1%; Score 6; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 162 SFLSNL 167
Db 3 SFLSNL 8

RESULT 52

US-08-822-830B-4

; Sequence 4, Application US/08822830B

; Patent No. 5871734

; GENERAL INFORMATION:

; APPLICANT: Lobb, Roy R.; Burkly, Linda C.

; TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/822,830B

; FILING DATE: 03-MAR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/456,193

; FILING DATE: 31-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/374,331

; FILING DATE: 18-JAN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/256,631

; FILING DATE: 12-JUL-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00030

; FILING DATE: 12-JAN-1993

; APPLICATION DATA:

; APPLICATION NUMBER: 07/821,768

; FILING DATE: 13-JAN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis (PLM)

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: BGP-021USCN

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 106 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-822-830B-4

Query Match

Best Local Similarity 2.1%; Score 6; DB 2; Length 106;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 TISTVQ 104

Db 74 TISTVQ 79

RESULT 54

US-09-157-452B-4

; Sequence 4, Application US/09157452B

; Patent No. 6482409

; GENERAL INFORMATION:

; APPLICANT: Lobb, Roy R.

; APPLICANT: Burkly, Linda C.

; TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE

; FILE REFERENCE: 10274-004003

; CURRENT APPLICATION NUMBER: US/09/157,452B

; CURRENT FILING DATE: 1998-09-21

; PRIOR APPLICATION NUMBER: US 08/950,660
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 08/373,857
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/284,603
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: PCT/US93/00924
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: US 07/835,139
; PRIOR FILING DATE: 1992-02-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-157-452B-4

Query Match 2.1%; Score 6; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 TISTVQ 104
| | | | |
Db 74 TISTVQ 79

RESULT 55
US-08-454-899G-10
; Sequence 10, Application US/08454899G
; Patent No. 6602503
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Carr, Philip J.
; APPLICANT: Tempest, Philip R.
; TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
; FILE REFERENCE: 10274-007001
; CURRENT APPLICATION NUMBER: US/08/454,899G
; CURRENT FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/004,798
; PRIOR FILING DATE: 1993-01-12
; PRIOR APPLICATION NUMBER: PCT/US94/00266
; PRIOR FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region
US-08-454-899G-10

Query Match 2.1%; Score 6; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 TISTVQ 104
| | | | |
Db 74 TISTVQ 79

RESULT 56
PCT-US93-00030-4
; Sequence 4, Application PC/TUS9300030
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; TITLE OF INVENTION: Treatment for Asthma
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago

; STATE: IL
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00030
; FILING DATE: 19930112
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,307-A; D002 CIP PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-00030-4

Query Match 2.1%; Score 6; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 TISTVQ 104
| | | | |
Db 74 TISTVQ 79

RESULT 57
PCT-US93-00924-4
; Sequence 4, Application PC/TUS9300924
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00924
; FILING DATE: 19930202
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-00924-4

Query Match 2.1%; Score 6; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 TISTVQ 104
Db 74 TISTVQ 79

RESULT 58
US-09-621-976-5264
; Sequence 5264, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5264
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -14...-1
; NAME/KEY: UNSURE
; LOCATION: 47
; OTHER INFORMATION: Xaa = Ala,Ser,Thr
; NAME/KEY: UNSURE
; LOCATION: 2,40
; OTHER INFORMATION: Xaa = Ala,Thr
; NAME/KEY: UNSURE
; LOCATION: 71
; OTHER INFORMATION: Xaa = Arg,Ser
; NAME/KEY: UNSURE
; LOCATION: 3
; OTHER INFORMATION: Xaa = Asp,Gly
; NAME/KEY: UNSURE
; LOCATION: 80
; OTHER INFORMATION: Xaa = Cys,Tyr
; NAME/KEY: UNSURE
; LOCATION: 4
; OTHER INFORMATION: Xaa = Gly,Ser
; NAME/KEY: UNSURE
; LOCATION: 8
; OTHER INFORMATION: Xaa = His,Gln
; NAME/KEY: UNSURE
; LOCATION: 70
; OTHER INFORMATION: Xaa = His,Gln,Arg
; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa = Pro,Gln
; NAME/KEY: UNSURE
; LOCATION: 61
; OTHER INFORMATION: Xaa = Pro,Thr

US-09-621-976-5264

Query Match 2.1%; Score 6; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QRVAAH 125
Db 37 QRVAAH 42

RESULT 59

US-09-134-001C-5132
; Sequence 5132, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5132
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5132

Query Match 2.1%; Score 6; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IYQGGI 247
Db 83 IYQGGI 88

RESULT 60

US-09-489-039A-9835
; Sequence 9835, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9835
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9835

Query Match 2.1%; Score 6; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 NISPLV 114
Db 6 NISPLV 11

RESULT 61

US-08-635-886C-248
; Sequence 248, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555

```
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 119
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-248

Query Match          2.1%; Score 6; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      83 GAFLVG 88

RESULT 62
US-08-974-690C-248
; Sequence 248, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 119
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-248

Query Match          2.1%; Score 6; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      83 GAFLVG 88

RESULT 63
US-08-635-886C-240
; Sequence 240, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 240
; LENGTH: 128
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-240

Query Match          2.1%; Score 6; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      92 GAFLVG 97

RESULT 64
US-08-974-690C-240
; Sequence 240, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 128
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-240

Query Match          2.1%; Score 6; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 GAFLVG 281
Db      92 GAFLVG 97

RESULT 65
US-09-134-000C-3666
; Sequence 3666, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3666
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3666

Query Match          2.1%; Score 6; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 116 ERGPQR 121
 Db 59 ERGPQR 64

RESULT 66

US-09-252-991A-18565
 ; Sequence 18565, Application US/09252991A
 ; Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18565

LENGTH: 134

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18565

Query Match 2.1%; Score 6; DB 4; Length 134;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 TGTGR 132
 Db 50 TGTGR 55

RESULT 67

US-09-252-991A-22722

; Sequence 22722, Application US/09252991A

; Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22722

LENGTH: 135

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22722

Query Match 2.1%; Score 6; DB 4; Length 135;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 PNDEES 72
 Db 40 PNDEES 45

RESULT 68

US-09-252-991A-27904

; Sequence 27904, Application US/09252991A

; Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27904

LENGTH: 135

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27904

Query Match

Best Local Similarity 100.0%; Score 6; DB 4; Length 135;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GTRGRS 133
 Db 69 GTRGRS 74

RESULT 69

US-09-328-352-4265

; Sequence 4265, Application US/09328352

; Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4265

LENGTH: 137

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-4265

Query Match

Best Local Similarity 100.0%; Score 6; DB 4; Length 137;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ERGPQR 121
 Db 101 ERGPQR 106

RESULT 70

US-09-134-001C-3776

; Sequence 3776, Application US/09134001C

; Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3776

LENGTH: 138

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3776

Query Match 2.1%; Score 6; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 KNEKAL 147
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Db 15 KNEKAL 20

RESULT 71

US-09-134-000C-6375
; Sequence 6375, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6375
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Enterococcus faecalis

US-09-134-000C-6375

Query Match 2.1%; Score 6; DB 4; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 ETISTV 103
| | | | |
Db 34 ETISTV 39

RESULT 72

US-09-593-887-8
; Sequence 8, Application US/09593887
; Patent No. 6607914
; GENERAL INFORMATION:
; APPLICANT: Belyavsky, Alexander
; APPLICANT: Popsueva, Anna
; APPLICANT: Luchinskaya, Natalia
; TITLE OF INVENTION: CAMELLO GENE FAMILY AND USES THEREOF
; FILE REFERENCE: 63475/258
; CURRENT APPLICATION NUMBER: US/09/593,887
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/333,229
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-593-887-8

Query Match 2.1%; Score 6; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 KALGRK 150
| | | | |
Db 101 KALGRK 106

RESULT 73

US-09-134-001C-3901
; Sequence 3901, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3901
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3901

Query Match 2.1%; Score 6; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 SVTNEH 264
| | | | |
Db 65 SVTNEH 70

RESULT 74

US-09-461-325-458
; Sequence 458, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 458
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-461-325-458

Query Match 2.1%; Score 6; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 128 GTRGRS 133
| | | | |
Db 43 GTRGRS 48

RESULT 75

US-10-012-542-458


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; Sequence 458, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 458
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-542-458
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Query Match          2.1%; Score 6; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 128 GTRGRS 133
Db 43 GTRGRS 48
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Job time : 25 secs
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:23:46 ; Search time 46 Seconds
(without alignments)

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Title: US-10-662-429-2

Perfect score: 281

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7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	281	100.0	281	8	US-08-971-317A-8
3	281	100.0	281	9	US-08-813-329-17
4	281	100.0	281	9	US-08-133-663-8
5	281	100.0	281	9	US-09-934-465-1
6	281	100.0	281	10	US-09-919-039-118
7	281	100.0	281	12	US-10-202-062-20
8	281	100.0	281	12	US-10-662-429-2
9	281	100.0	281	12	US-10-662-430-2
10	281	100.0	281	12	US-10-662-431-2
11	281	100.0	281	13	US-10-039-785-66
12	281	100.0	281	13	US-10-011-125-4
13	281	100.0	281	13	US-10-001-054-54
14	281	100.0	281	14	US-10-093-766-54
15	281	100.0	281	14	US-10-174-654-11
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					Sequence 8, Appli
					Sequence 17, Appli
					Sequence 4, Appli
					Sequence 118, Appli
					Sequence 20, Appli
					Sequence 2, Appli
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					Sequence 66, Appli
					Sequence 4, Appli
					Sequence 54, Appli
					Sequence 54, Appli
					Sequence 11, Appli

16	281	100.0	281	14	US-10-151-882-41	Sequence 41, Appli
17	281	100.0	281	14	US-10-218-547-20	Sequence 20, Appli
18	281	100.0	281	14	US-10-322-673-72	Sequence 72, Appli
19	281	100.0	281	14	US-10-139-785-66	Sequence 66, Appli
20	281	100.0	281	14	US-10-310-793-26	Sequence 26, Appli
21	281	100.0	281	15	US-10-292-486-5	Sequence 5, Appli
22	281	100.0	281	15	US-10-333-712-1	Sequence 1, Appli
23	279	99.3	279	13	US-10-066-209-3	Sequence 3, Appli
24	193	68.7	208	9	US-09-855-544A-16	Sequence 16, Appli
25	187	66.5	461	12	US-10-389-223A-6	Sequence 6, Appli
26	187	66.5	480	12	US-10-389-223A-4	Sequence 4, Appli
27	187	66.5	614	12	US-10-389-223A-2	Sequence 2, Appli
28	168	59.8	168	9	US-09-900-530A-10	Sequence 10, Appli
29	166	59.1	166	9	US-09-779-050A-16	Sequence 16, Appli
30	161	57.3	161	14	US-10-216-074-7	Sequence 7, Appli
31	161	57.3	161	14	US-10-338-083-11	Sequence 11, Appli
32	156	55.5	236	14	US-10-185-425-5	Sequence 5, Appli
33	141	50.2	246	9	US-09-855-544A-13	Sequence 13, Appli
34	127	45.2	164	13	US-10-116-378-29	Sequence 29, Appli
35	107	38.1	113	9	US-09-855-544A-15	Sequence 15, Appli
36	105	37.4	188	9	US-09-855-544A-14	Sequence 14, Appli
37	90	32.0	98	9	US-09-855-544A-10	Sequence 10, Appli
38	87	31.0	88	9	US-09-855-544A-9	Sequence 9, Appli
39	85	30.2	83	14	US-10-286-696-12	Sequence 12, Appli
40	56	19.9	56	15	US-10-399-018-20	Sequence 20, Appli
41	44	15.7	50	9	US-09-864-761-33427	Sequence 33427, A
42	44	15.7	52	9	US-09-855-544A-11	Sequence 11, Appli
43	44	15.7	55	9	US-09-855-544A-12	Sequence 12, Appli
44	34	12.1	34	14	US-10-272-411-24	Sequence 24, Appli
45	34	12.1	34	14	US-10-272-328A-24	Sequence 24, Appli
46	14	5.0	172	9	US-09-779-050A-17	Sequence 17, Appli
47	14	5.0	291	10	US-09-873-829-6	Sequence 6, Appli
48	14	5.0	291	13	US-10-017-910-6	Sequence 6, Appli
49	12	4.3	87	14	US-10-286-696-13	Sequence 13, Appli
50	11	3.9	21	15	US-10-399-018-21	Sequence 21, Appli
51	10	3.6	10	14	US-10-272-411-25	Sequence 25, Appli
52	10	3.6	10	14	US-10-272-328A-25	Sequence 25, Appli
53	9	3.2	9	14	US-10-272-411-27	Sequence 27, Appli
54	9	3.2	9	14	US-10-272-328A-27	Sequence 27, Appli
55	7	2.5	10	14	US-10-360-836-71	Sequence 71, Appli
56	7	2.5	42	12	US-10-424-599-25595	Sequence 25595, A
57	7	2.5	42	12	US-10-424-599-263624	Sequence 263624, A
58	7	2.5	60	12	US-10-424-599-258329	Sequence 258329, A
59	7	2.5	112	12	US-10-424-599-143535	Sequence 143535, A
60	7	2.5	117	12	US-10-424-599-186624	Sequence 186624, A
61	7	2.5	125	14	US-10-103-313-421	Sequence 421, Appli
62	7	2.5	170	12	US-10-424-599-235009	Sequence 235009, A
63	7	2.5	184	12	US-10-424-599-164595	Sequence 164595, A
64	7	2.5	196	12	US-10-425-114-64832	Sequence 64832, A
65	7	2.5	200	14	US-10-178-055-4	Sequence 4, Appli
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67	7	2.5	240	9	US-09-997-165-2	Sequence 2, Appli
68	7	2.5	241	9	US-09-925-301-1105	Sequence 1105, Appli
69	7	2.5	247	14	US-10-145-602-4	Sequence 4, Appli
70	7	2.5	267	12	US-10-424-599-276617	Sequence 276617, A
71	7	2.5	418	9	US-09-808-483-18	Sequence 18, Appli
72	7	2.5	420	15	US-10-369-493-1984	Sequence 1984, Appli
73	7	2.5	429	15	US-10-282-132A-54850	Sequence 54850, A
74	7	2.5	429	15	US-10-312-273-227	Sequence 227, Appli
75	7	2.5	429	15	US-10-286-762-189	Sequence 189, Appli
76	7	2.5	474	14	US-10-156-761-11437	Sequence 11437, A
77	7	2.5	531	12	US-10-425-114-46560	Sequence 46560, A
78	7	2.5	552	14	US-10-236-433-16	Sequence 16, Appli
79	7	2.5	574	14	US-10-236-433-2	Sequence 2, Appli
80	7	2.5	758	15	US-10-108-260A-2713	Sequence 2713, Appli
81	7	2.5	942	12	US-10-425-114-68187	Sequence 68187, A
82	7	2.5	1009	14	US-10-156-761-13813	Sequence 13813, A
83	7	2.5	1084	13	US-10-024-623-23	Sequence 23, Appli
84	7	2.5	1084	14	US-10-154-419-73	Sequence 73, Appli
85	7	2.5	1084	14	US-10-146-733-68	Sequence 68, Appli
86	7	2.5	1095	13	US-10-024-623-26	Sequence 26, Appli
87	7	2.5	1095	13	US-10-024-623-36	Sequence 36, Appli
88	7	2.5	1095	14	US-10-154-419-76	Sequence 76, Appli

89 7 2.5 1095 14 US-10-154-419-86 Sequence 86, Appl
 90 7 2.5 1095 14 US-10-146-733-71 Sequence 71, Appl
 91 7 2.5 1095 14 US-10-146-733-81 Sequence 81, Appl
 92 7 2.5 1847 15 US-10-369-493-1075 Sequence 1075, Ap
 93 7 2.5 1981 9 US-09-928-457-38 Sequence 38, Appl
 94 7 2.5 2015 12 US-10-282-122A-65772 Sequence 65772, A
 95 7 2.5 2015 14 US-10-066-551-1 Sequence 1, Appl
 96 6 2.1 6 14 US-10-272-411-26 Sequence 26, Appl
 97 6 2.1 6 14 US-10-272-328A-26 Sequence 26, Appl
 98 6 2.1 14 9 US-09-900-530A-19 Sequence 19, Appl
 99 6 2.1 22 9 US-09-864-761-34476 Sequence 34476, A
 100 6 2.1 23 10 US-09-776-724A-187 Sequence 187, App

ALIGNMENTS

RESULT 1
 US-08-916-625B-6
 ; Sequence 6, Application US/08916G25B
 ; Publication No. US20010010924A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DEEN, KRITH C.
 ; APPLICANT: YOUNG, PETER R.
 ; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
 ; TITLE OF INVENTION: RECEPTOR, TR6
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RATNER & PRESTIA
 ; STREET: P.O. BOX 980
 ; CITY: VALLEY FORGE
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/916,625B
 ; FILING DATE: 22-AUG-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/853,684
 ; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: 60/041,230
 ; FILING DATE: 14-MARCH-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PRESTIA, PAUL F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GH-50008-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-916-625B-6

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDNDSESMNSPCQVQKWQLRQVRKMLRTSETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDNDSESMNSPCQVQKWQLRQVRKMLRTSETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 QY 181 FYIYSOTYFRFOEIKENTKNDKQVQYIYKTSYVDPDILLMKSAENSCWSKDAEYGLY 240
 DB 181 FYIYSOTYFRFOEIKENTKNDKQVQYIYKTSYVDPDILLMKSAENSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 2

US-08-971-317A-8
 ; Sequence 8, Application US/08971317A
 ; Publication No. US20010010925A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/971,317A
 ; FILING DATE: 17-NOV-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goller, Mimi C
 ; REGISTRATION NUMBER: 39,046
 ; REFERENCE/DOCKET NUMBER: 6255.US.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (847) 935-7550
 ; TELEFAX: (847) 938-2623
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. US20010010925A1e
 ; US-08-971-317A-8

Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDNDSESMNSPCQVQKWQLRQVRKMLRTSETISTVQEKQONISPLVRERGPO 120
 DB 61 DDSYWDNDSESMNSPCQVQKWQLRQVRKMLRTSETISTVQEKQONISPLVRERGPO 120

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QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 3

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US-09-813-329-17
; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-17
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Query Match 100.0%; Score 281; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEQQNISPVLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEQQNISPVLVRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 4

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US-09-193-663-8
; Sequence 8, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; PRIOR FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8
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Query Match 100.0%; Score 281; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEQQNISPVLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEQQNISPVLVRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 5

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US-09-934-465-1
; Sequence 1, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1
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Query Match 100.0%; Score 281; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEQQNISPVLVRGPQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEQQNISPVLVRGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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Db 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Qy 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Qy 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
 Qy 241 SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFVLG 281
 Db 241 SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 9

US-10-662-430-2
 ; Sequence 2, Application US/10662430
 ; Publication No. US20040048340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662,430
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF261
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-430-2

Query Match 100.0%; Score 281; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Qy 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120

Qy 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 Qy 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
 Qy 241 SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFVLG 281
 Db 241 SIYQGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 10

US-10-662-431-2
 ; Sequence 2, Application US/10662431
 ; Publication No. US20040047864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662,431
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF261
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-431-2

Query Match 100.0%; Score 281; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMVEVGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Qy 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Db 61 DSDYWDNDDESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Qy 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 11

US-10-039-785-66
; Sequence 66, Application US/10039785
; Publication No. US2002067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66

Query Match 100.0%; Score 281; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACPLKE 60
DB 1 MAMMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACPLKE 60
QY 61 DDSYDPNDEESMNSPCWQVQWQRLVVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYDPNDEESMNSPCWQVQWQRLVVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 12

US-10-011-125-4

; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: F1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-125-4
Query Match 100.0%; Score 281; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACPLKE 60
DB 1 MAMMEVGGPSLGGTCTVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSKSGIACPLKE 60
QY 61 DDSYDPNDEESMNSPCWQVQWQRLVVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYDPNDEESMNSPCWQVQWQRLVVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHKG 180
DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHKG 180
QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSAKNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 13

US-10-001-054-54
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabatoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001,054
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29

;; PRIOR APPLICATION NUMBER: 60/085149
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/090691
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/096891
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 60/096894
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100263
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/101476
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/107783
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112420
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/115554
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/116533
;; PRIOR FILING DATE: 1999-01-20
;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/131294
;; PRIOR FILING DATE: 1999-04-07
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
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;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/162506
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;; PRIOR APPLICATION NUMBER: 60/170262
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;; PRIOR FILING DATE: 2000-06-05
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;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-11-19
;; PRIOR APPLICATION NUMBER: 09/218517
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 09/284291
;; PRIOR FILING DATE: 1999-04-12
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
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;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380913
;; PRIOR FILING DATE: 1999-09-09
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/866034
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/882636
;; PRIOR FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 09/924419
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/927796
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: PCT/US98/18824
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/US99/00106
;; PRIOR FILING DATE: 1999-01-05
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/08615
;; PRIOR FILING DATE: 1999-04-20
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28634
;; PRIOR FILING DATE: 1999-12-01
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00376
;; PRIOR FILING DATE: 2000-01-06
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04342
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/06884
;; PRIOR FILING DATE: 2000-03-15
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: PCT/US00/13705
;; PRIOR FILING DATE: 2000-05-17
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/14941
;; PRIOR FILING DATE: 2000-05-30
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/22031
;; PRIOR FILING DATE: 2000-08-11
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/06666
 ; PRIOR FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/17092
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: PCT/US01/17800
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21066
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: PCT/US01/27099
 ; PRIOR FILING DATE: 2001-08-29
 ; NUMBER OF SEQ ID NOS: 91
 ; SEQ ID NO 54
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-001-054-54

Query Match 100.0%; Score 281; DB 13; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273; Indels 0; Gaps 0;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120
 DB 61 DSYWDPNDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
 US-10-093-766-54
 ; Sequence 54; Application US/10093766
 ; Publication No. US20030013099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lasek, Amy W.
 ; APPLICANT: Jones, David A.
 ; APPLICANT: Karpf, Adam R.
 ; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
 ; FILE REFERENCE: PA-0047 US
 ; CURRENT APPLICATION NUMBER: US/10/093,766
 ; CURRENT FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 54
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
 US-10-093-766-54

Query Match 100.0%; Score 281; DB 14; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273; Indels 0; Gaps 0;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120
 DB 61 DSYWDPNDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240
 DB 181 FYIYSQTYFRFQBEIKENTKNDKQVQIYKYTSYDPDILLMKSARNCSWKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15
 US-10-174-654-11
 ; Sequence 11; Application US/10174654
 ; Publication No. US20030044937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bienkowski, Michael J
 ; Mills, Cynthia J
 ; Jones, David A
 ; TITLE OF INVENTION: TNF-Related Death Ligand
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
 ; STREET: 301 Henrietta Street
 ; CITY: Kalamazoo
 ; STATE: MI
 ; COUNTRY: USA
 ; ZIP: 49001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 Diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/174,654
 ; FILING DATE: 19-Jun-2002
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kerber, Lori L.
 ; REGISTRATION NUMBER: 41,113
 ; REFERENCE/DOCKET NUMBER: 6111.N CN1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 616/833-0974
 ; TELEFAX: 616/833-8897
 ; TELEX: 224401
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-10-174-654-11

Query Match 100.0%; Score 281; DB 14; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.2e-273; Indels 0; Gaps 0;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATYVYFTNELKQMDKYSGIACFLKE 60

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Db 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
Db 61 DSDYDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
QY 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240
Db 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 16
US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-41
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Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
Db 61 DSDYDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
QY 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240
Db 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 17
US-10-218-547-20
; Sequence 20, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
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; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20
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Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
Db 61 DSDYDNDDESMNSPCWQVKWQLRQLVRKMLTSETISTVQEKQONISPLVRERGPO 120
QY 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RAAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240
Db 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 18
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72
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Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYNDPNDDESMNPFQWQKQLRQVVKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DSDYNDPNDDESMNPFQWQKQLRQVVKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 19

US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

; FILE REFERENCE: PF550

; CURRENT APPLICATION NUMBER: US/10/139,785

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: 60/369,860

; PRIOR FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 60/341,237

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 60/331,310

; PRIOR FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/331,044

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 60/327,364

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/323,807

; PRIOR FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/309,176

; PRIOR FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 60/294,981

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/293,473

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 66

; LENGTH: 281

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-139-785-66

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYNDPNDDESMNPFQWQKQLRQVVKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DSDYNDPNDDESMNPFQWQKQLRQVVKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
DB 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 20

US-10-310-793-26

; Sequence 26, Application US/10310793

; Publication No. US20030198640A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A

; APPLICANT: Zhang, Jun

; APPLICANT: Wei, Ping

; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Disease:

; FILE REFERENCE: PF573

; CURRENT APPLICATION NUMBER: US/10/310,793

; PRIOR FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 60/336,695

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 10/226,294

; PRIOR FILING DATE: 2002-08-23

; PRIOR APPLICATION NUMBER: 60/314,381

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 09/899,059

; PRIOR FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: 60/278,449

; PRIOR FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: 60/216,879

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 09/559,290

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/180,908

; PRIOR FILING DATE: 2000-02-08

; PRIOR APPLICATION NUMBER: 60/134,067

; PRIOR FILING DATE: 1999-05-13

; PRIOR APPLICATION NUMBER: 60/132,227

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26

; LENGTH: 281

; TYPE: PRT

; ORGANISM: human

US-10-310-793-26

Query Match 100.0%; Score 281; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMVEVQGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYNDPNDDESMNPFQWQKQLRQVVKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DSDYNDPNDDESMNPFQWQKQLRQVVKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWSDAEYGLY 240

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Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 21
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532P1
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-486-5

Query Match 100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Qy 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 22
US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US20040005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique

Query Match 99.3%; Score 279; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.2e-271;
```

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; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1838R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-333-712-1

Query Match 100.0%; Score 281; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-273;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTQCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
Qy 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
Qy 241 SIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 23
US-10-066-209-3
; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3

Query Match 99.3%; Score 279; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.2e-271;
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Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVQGSLSGTCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKGIACFLKEDD 62
DB 1 MMEVQGSLSGTCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKGIACFLKEDD 60

QY 63 SYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQRV 122
DB 61 SYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQRV 120

QY 123 RAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKGFY 182
DB 121 AAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKGFY 180

QY 183 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLYSI 242
DB 181 YIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLYSI 240

QY 243 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 YGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 24
US-09-855-544A-16
; Sequence 16, Application US/09855544A
; Patent No. US2002006125A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match 68.7%; Score 193; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.4e-185;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGSLSGTCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKGIACFLKE 60
DB 1 MAMMEVQGSLSGTCVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGKGIACFLKE 60

QY 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DSYWDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120

QY 121 RVAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
DB 121 RVAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQ 193
DB 181 FYIYSQTYFRFQ 193

RESULT 25
US-10-389-223A-6
; Sequence 6, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wuest, Harald
; APPLICANT: Moosmayer, Dieter
; TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokines
; TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)

FILE REFERENCE: 1708.002US1
CURRENT APPLICATION NUMBER: US/10/389,223A
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 461
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of sequence 6: synthetic amino acid sequence of an anti-body-cytokine AMAIZE fusion protein of the invention exempl
OTHER INFORMATION: TRAIL-AMAIZE (40)
FEATURE:
OTHER INFORMATION: Stop codon: NT 1384-1386
US-10-389-223A-6

Query Match 66.5%; Score 187; DB 12; Length 461;
Best Local Similarity 100.0%; Pred. No. 7.1e-179;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRERGPQRVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
DB 275 TSEETISTVQEKQONISPLVRERGPQRVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 334

QY 155 ESSRSGHSFSLNHLRNGELVHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKYT 214
DB 335 ESSRSGHSFSLNHLRNGELVHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKYT 394

QY 215 SYDPDPILLMKSARNSCWSDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
DB 395 SYDPDPILLMKSARNSCWSDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASF 454

QY 275 FGAFVLG 281
DB 455 FGAFVLG 461

RESULT 26
US-10-389-223A-4
; Sequence 4, Application US/10389223A
; Publication No. US20040033511A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; APPLICANT: Moosmayer, Dieter
; TITLE OF INVENTION: Site-specific Antibody-mediated Activation of Proapoptotic Cytokines
; TITLE OF INVENTION: AMAIZE (Antibody-mediated Apoptosis Inducing Cytokines)
; FILE REFERENCE: 1708.002US1
; CURRENT APPLICATION NUMBER: US/10/389,223A
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of sequence 4: synthetic amino acid sequence of an anti-body-cytokine AMAIZE fusion protein of the invention exempl
OTHER INFORMATION: TRAIL-AMAIZE (OS4)
FEATURE:
OTHER INFORMATION: Stop codon: NT 1441-1443
US-10-389-223A-4

Query Match 66.5%; Score 187; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 7.3e-179;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVRERGPQRVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 154
DB 294 TSEETISTVQEKQONISPLVRERGPQRVAAHITGTRGSRNTLSSPNSKNEKALGRKINSW 353

155 ESSRSGHSFLNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVYIYKYT 214
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TITLE OF INVENTION: Combination and Use in Gene Therapy
FILE REFERENCE: 5006-1-002
CURRENT APPLICATION NUMBER: US/09/900,530A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 168
TYPE: PRT
ORGANISM: homo sapiens
US-09-900-530A-10

Query Match 59.8%; Score 168; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.4e-160;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 114 VREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGE 173
Db 1 VREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGE 60
Qy 174 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQMVYIYKYTSDPILLMKSRNSCWSK 233
Db 61 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQMVYIYKYTSDPILLMKSRNSCWSK 120
Qy 234 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 121 DAEGYLSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168

RESULT 29
US-09-779-050A-16
Sequence 16, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-050A-16

Query Match 59.1%; Score 166; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.4e-158;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 116 ERGQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELV 175
Db 1 ERGQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHLRNGELV 60
Qy 176 IHEKGFYIYSQTYFRFOEIKENTKNDKQMVYIYKYTSDPILLMKSRNSCWSKDA 235
Db 61 IHEKGFYIYSQTYFRFOEIKENTKNDKQMVYIYKYTSDPILLMKSRNSCWSKDA 120
Qy 236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 121 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166

RESULT 30
US-10-216-074-7
Sequence 7, Application US/10216074
Publication No. US2003014845A1

Query Match 66.5%; Score 187; DB 12; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.1e-179;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 95 TSEETISVQEQKQNISPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 154
Db 428 TSEETISVQEQKQNISPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 487
Qy 155 ESSRSGHSFLNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVYIYKYT 214
Db 488 ESSRSGHSFLNLHLRNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQMVYIYKYT 547
Qy 215 SYDPILLMKSRNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 274
Db 548 SYDPILLMKSRNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 607
Qy 275 FGAFVLG 281
Db 608 FGAFVLG 614

RESULT 28
US-09-900-530A-10
Sequence 10, Application US/09900530A
Patent No. US20020128438A1
GENERAL INFORMATION:
APPLICANT: Seol, Dae-Wu
APPLICANT: Billiar, Timothy R.
TITLE OF INVENTION: DNA Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their


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; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-7

Query Match      57.3%; Score 161; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 3.5e-153;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 60

Qy 181 FYIYISQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARNCSWKDAEYGLY 240
Db 61 FYIYISQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARNCSWKDAEYGLY 120

Qy 241 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
Db 121 SIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 31
US-10-338-083-11
; Sequence 11, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Taneey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match      57.3%; Score 161; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 3.5e-153;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEK 179
Db 1 QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEK 60

Qy 180 GFYIYISQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARNCSWKDAEYGL 239
Db 61 GFYIYISQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARNCSWKDAEYGL 120
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Qy 240 YSIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 280
Db 121 YSIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 32
US-10-185-425-5
; Sequence 5, Application US/10185425
; Publication No. US20030053984A1
; GENERAL INFORMATION:
; APPLICANT: Apotech Research and Development Ltd.
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Holler, Nils
; TITLE OF INVENTION: A Dimer or an Oligomer of a Dimer, Trimer, Tetramer, or Pentamer
; TITLE OF INVENTION: Recombinant Fusion Proteins
; FILE REFERENCE: 1708.001US1
; CURRENT APPLICATION NUMBER: US/10/185,425
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/EP00/13032
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: DE 199 63 859.4
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TRAIL-ACRP30
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(8)
; OTHER INFORMATION: Flag
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (9)...(16)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17)...(108)
; OTHER INFORMATION: mouseACRP30 aa 18-111
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (109)...(110)
; OTHER INFORMATION: Linker
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (111)...(296)
; OTHER INFORMATION: humanTRAIL aa 95-281
US-10-185-425-5

Query Match      55.5%; Score 156; DB 14; Length 296;
Best Local Similarity 100.0%; Pred. No. 6.2e-148;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFYIY 185
Db 141 ITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKGFYIY 200

Qy 186 SOTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARNCSWKDAEYGLYIYQG 245
Db 201 SOTYFRFQEEIKENTKNDKQVQIYKYTSYPPDPILLMKARNCSWKDAEYGLYIYQG 260

Qy 246 GIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 281
Db 261 GIFELKENDRIFSVTNEHLIDMDHEASFFGAFVLG 296

RESULT 33
US-09-855-544A-13
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; Sequence 13, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-13

Query Match      50.2%; Score 141; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 5.9e-133;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      141 SKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKGFIYIYSQTYFRFOEIKENT 200
Db      141 SKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKGFIYIYSQTYFRFOEIKENT 165

Qy      201 KNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLYSIYGGIFELKENDRIFVSV 260
Db      201 KNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEYGLYSIYGGIFELKENDRIFVSV 225

Qy      261 TNEHLIDMDHEASFFGAFVNG 281
Db      261 TNEHLIDMDHEASFFGAFVNG 246

RESULT 34
US-10-116-378-29
; Sequence 29, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206K1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29

Query Match      45.2%; Score 127; DB 13; Length 164;
Best Local Similarity 100.0%; Pred. No. 4.6e-119;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      118 GPQVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEH 177
Db      1 GPQVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEH 60

Qy      178 EKGFIYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEY 237
Db      61 EKGFIYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWCKDAEY 120
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Qy      238 GLYSIQ 244
Db      121 GLYSIQ 127

RESULT 35
US-09-855-544A-15
; Sequence 15, Application US/098555544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-15

Query Match      38.1%; Score 107; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.9e-99;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy      61 DDSYDNDPDEESMNSPCWQVQKWLQRLVVRKMLRTSEETISTVQEQ 107
Db      61 DDSYDNDPDEESMNSPCWQVQKWLQRLVVRKMLRTSEETISTVQEQ 107

RESULT 36
US-09-855-544A-14
; Sequence 14, Application US/098555544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-14

Query Match      37.4%; Score 105; DB 9; Length 188;
Best Local Similarity 100.0%; Pred. No. 6.2e-97;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db      1 MANMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

Qy      61 DDSYDNDPDEESMNSPCWQVQKWLQRLVVRKMLRTSEETISTVQEQ 105
Db      61 DDSYDNDPDEESMNSPCWQVQKWLQRLVVRKMLRTSEETISTVQEQ 105

RESULT 37
US-09-855-544A-10
; Sequence 10, Application US/098555544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
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; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-10

Query Match      32.0%; Score 90; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 4e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQWKQQLRQLRK 90
DB 61 DDSYWDNDDESMNSPCQWKQQLRQLRK 90

RESULT 38
US-09-855-544A-9
; Sequence 9, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-9

Query Match      31.0%; Score 87; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.7e-79;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCQWKQQLRQLRK 87
DB 61 DDSYWDNDDESMNSPCQWKQQLRQLRK 87

RESULT 39
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Heu, Hailing
; APPLICANT: Boyle, William J
; APPLICANT: Wooden, Scott K
; TITLE OF INVENTION: Fhm, A No. US20030129706A1el Member of the TNF Ligand Super-gene
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
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; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-696-12

Query Match      30.2%; Score 85; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.6e-77;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 ERGPQVAAHITGTRGRSNTLSSPNSKNEKALCRKINSWESSRSGHSFSLNHLRNGELV 175
DB 1 ERGPQVAAHITGTRGRSNTLSSPNSKNEKALCRKINSWESSRSGHSFSLNHLRNGELV 60
QY 176 IHEKGFYIYSQTYFRFOEIKENT 200
DB 61 IHEKGFYIYSQTYFRFOEIKENT 85

RESULT 40
US-10-399-018-20
; Sequence 20, Application US/10399018
; Publication No. US20040002118A1
; GENERAL INFORMATION:
; APPLICANT: Smilansky, Zeev
; TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
; FILE REFERENCE: 9124.137USWO
; CURRENT APPLICATION NUMBER: US/10/399,018
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/IL01/00944
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: IL138946
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-018-20

Query Match      19.9%; Score 56; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.2e-48;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RTSETISTVQEKQONISPLVREGRGPQVAAHITGTRGRSNTLSSPNSKNEKALGR 149
DB 1 RTSETISTVQEKQONISPLVREGRGPQVAAHITGTRGRSNTLSSPNSKNEKALGR 56

RESULT 41
US-09-864-761-33427
; Sequence 33427, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33427
LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007051.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P50591, EVALUE 3.00e-19
OTHER INFORMATION: EST_HUMAN HIT: AUI34224.1, EVALUE 1.00e-18
OTHER INFORMATION: EST_HUMAN HIT: H54628.1, EVALUE 3.00e-18
US-09-864-761-33427

Query Match 15.7%; Score 44; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.2e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQ 44
DB 2 MANMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQ 45

RESULT 42
US-09-855-544A-11
Sequence 11, Application US/09855544A
Patent No. US20020061525A1
GENERAL INFORMATION:
APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-544A-11

Query Match 15.7%; Score 44; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQ 44
DB 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQ 44

RESULT 43
US-09-855-544A-12
Sequence 12, Application US/09855544A
Patent No. US20020061525A1
GENERAL INFORMATION:
APPLICANT: Rodrigo YELIN et al.
TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
FILE REFERENCE: 2786-0173P
CURRENT APPLICATION NUMBER: US/09/855,544A
CURRENT FILING DATE: 2001-05-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-544A-12

Query Match 15.7%; Score 44; DB 9; Length 55;
Best Local Similarity 100.0%; Pred. No. 3.4e-36;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQ 44
DB 1 MANMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYVFTNELKQ 44

RESULT 44
US-10-272-411-24
Sequence 24, Application US/10272411
Publication No. US20030100068A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-411-24

Query Match 12.1%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 162
DB 1 TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS 34

RESULT 45
US-10-272-328A-24
Sequence 24, Application US/10272328A
Publication No. US20030109444A1

```
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-24

Query Match      12.1%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.4e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      129 TGRSNTLSSPNKNEKALGRKINSWESSRSQHS 162
Db      1  TGRSNTLSSPNKNEKALGRKINSWESSRSQHS 34

RESULT 46
US-09-779-050A-17
; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match      5.0%; Score 14; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      207 VQYIKYKTSYPDPI 220
Db      98 VQYIKYKTSYPDPI 111

RESULT 47
US-09-873-829-6
; Sequence 6, Application US/09873829
; Publication No. US20030185820A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; APPLICANT: Wong, Brian
; APPLICANT: Josien, Regis
; APPLICANT: Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
```

```
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/873,829
; FILING DATE: 04-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,115
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200 CIP N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-873-829-6

Query Match      5.0%; Score 14; DB 10; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      207 VQYIKYKTSYPDPI 220
Db      217 VQYIKYKTSYPDPI 230

RESULT 48
US-10-017-910-6
; Sequence 6, Application US/10017910
; Publication No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; APPLICANT: Wong, Brian
; APPLICANT: Josien, Regis
; APPLICANT: Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

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; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-017-910-6

Query Match 5.0%; Score 14; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 VQYIYKYSYPDI 220
Db 217 VQYIYKYSYPDI 230

RESULT 49
US-10-286-696-13
; Sequence 13, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Heu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. US20030129706A1 Member of the TNF Ligand Superfamily
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-10-286-696-13

Query Match 4.3%; Score 12; DB 14; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 YIYQTYFRFQE 194
Db 65 YIYQTYFRFQE 76

RESULT 50
US-10-399-018-21
; Sequence 21, Application US/10399018
; Publication No. US20040002118A1
; GENERAL INFORMATION:
; APPLICANT: Smilansky, Zeev
```

```
; TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
; FILE REFERENCE: 9124.137USWO
; CURRENT APPLICATION NUMBER: US/10/399,018
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/IL01/00944
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: IL138946
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-018-21

Query Match 3.9%; Score 11; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 RTSEETISTVQ 104
Db 1 RTSEETISTVQ 11

RESULT 51
US-10-272-411-25
; Sequence 25, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-411-25

Query Match 3.6%; Score 10; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKENTKN 202
Db 1 QEEIKENTKN 10

RESULT 52
US-10-272-328A-25
; Sequence 25, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-25

Query Match 3.6%; Score 10; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 193 QBEIKENTKN 202
Db 1 QBEIKENTKN 10
|||||

RESULT 53

US-10-272-411-27
; Sequence 27, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-411-27

Query Match 3.2%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 229 SCWSKDAEY 237
Db 1 SCWSKDAEY 9
|||||

RESULT 54

US-10-272-328A-27
; Sequence 27, Application US/10272328A
; Publication No. US2003010944A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-27

Query Match 3.2%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 SCWSKDAEY 237
Db 1 SCWSKDAEY 9
|||||

RESULT 55

US-10-360-836-71
; Sequence 71, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-71

Query Match 2.5%; Score 7; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 SKNEKAL 147
Db 2 SKNEKAL 8
|||||

RESULT 56

US-10-424-599-255595
; Sequence 255595, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255595
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72823C.1.pcp
US-10-424-599-255595

Query Match 2.5%; Score 7; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 EEIKENT 200
Db 12 EEIKENT 18
|||||

RESULT 57

US-10-424-599-263624

; Sequence 263624, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 263624
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80072C.1.pep
US-10-424-599-263624

Query Match 2.5%; Score 7; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 KRMILRT 95
Db 32 KRMILRT 38

RESULT 58
US-10-424-599-258329
; Sequence 258329, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 258329
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(60)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75296C.1.pep
US-10-424-599-258329

Query Match 2.5%; Score 7; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 KALGRKI 151
Db 37 KALGRKI 43

RESULT 59
US-10-424-599-143535
; Sequence 143535, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143535
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100626C.1.pep
US-10-424-599-143535

Query Match 2.5%; Score 7; DB 12; Length 112;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 KNEKALG 148
Db 97 KNEKALG 103

RESULT 60
US-10-424-599-186624
; Sequence 186624, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186624
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139534C.1.pep
US-10-424-599-186624

Query Match 2.5%; Score 7; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQLVR 89
Db 69 QLRQLVR 75

RESULT 61
US-10-103-313-421
; Sequence 421, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 421
; LENGTH: 125
; TYPE: PRT

ORGANISM: Homo sapiens
US-10-103-313-421

Query Match 2.5%; Score 7; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 HSFLSNL 167
Db 32 HSFLSNL 38

RESULT 62
US-10-424-599-235009
; Sequence 235009, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 235009
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_54241C.1.pep
US-10-424-599-235009

Query Match 2.5%; Score 7; DB 12; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 HSFLSNL 167
Db 127 HSFLSNL 133

RESULT 63
US-10-424-599-164595
; Sequence 164595, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164595
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119647C.1.pep
US-10-424-599-164595

Query Match 2.5%; Score 7; DB 12; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 PNSKNEK 145
Db 139 PNSKNEK 145

Db 118 PNSKNEK 124

RESULT 64

US-10-425-114-64832
; Sequence 64832, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64832
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4720-003-G12_FLI.pep
US-10-425-114-64832

Query Match 2.5%; Score 7; DB 12; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 SIYQGGI 247
Db 55 SIYQGGI 61

RESULT 65

US-10-178-055-4
; Sequence 4, Application US/10178055
; Publication No. US20030105008A1
; GENERAL INFORMATION:
; APPLICANT: Dutta, Anindya
; APPLICANT: Dhar, Suman
; TITLE OF INVENTION: GEMININ AND ORCIN INHIBIT REPLICATION OF HERPESVIRUSES, PAPILLOM
; TITLE OF INVENTION: AND POLYOMAVIRUSES
; FILE REFERENCE: B00801/70253(JRV/MXA)
; CURRENT APPLICATION NUMBER: US/10/178,055
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,963
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-178-055-4

Query Match 2.5%; Score 7; DB 14; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QBEIKEN 199
Db 9 QBEIKEN 15

RESULT 66

US-10-178-055-2
; Sequence 2, Application US/10178055
; Publication No. US20030105008A1
; GENERAL INFORMATION:

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; APPLICANT: Dutta, Anindya
; APPLICANT: Dhar, Suman
; TITLE OF INVENTION: GEMININ AND ORC3N INHIBIT REPLICATION OF HERPESVIRUSES, PAPILLOMA
; TITLE OF INVENTION: AND POLYOMAVIRUSES
; FILE REFERENCE: R00801/70253(JRV/MXA)
; CURRENT APPLICATION NUMBER: US/10/178,055
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,963
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-178-055-2

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 9 QEEIKEN 15

RESULT 67
US-09-997-165-2
; Sequence 2, Application US/09997165
; Patent No. US2002014199A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Fanslow, William C.
; TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF
; FILE REFERENCE: 2913-US
; CURRENT APPLICATION NUMBER: US/09/997,165
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: PCT/US00/14612
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,450
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-165-2

Query Match          2.5%; Score 7; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 NTLSSPN 140
Db 231 NTLSSPN 237

RESULT 68
US-09-925-301-1105
; Sequence 1105, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1105
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1105

Query Match          2.5%; Score 7; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QEEIKEN 199
Db 41 QEEIKEN 47

RESULT 69
US-10-145-602-4
; Sequence 4, Application US/10145602
; Publication No. US20030171563A1
; GENERAL INFORMATION:
; APPLICANT: McNamara, Peter
; TITLE OF INVENTION: REGULATORS OF BACTERIAL VIRULENCE FACTOR EXPRESSION
; FILE REFERENCE: KCC 4766
; CURRENT APPLICATION NUMBER: US/10/145,602
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/291,917
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-145-602-4

Query Match          2.5%; Score 7; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
Db 91 RIFVSVT 97

RESULT 70
US-10-424-599-276617
; Sequence 276617, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276617
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91804C.1.pep
US-10-424-599-276617

Query Match          2.5%; Score 7; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 HSFLSNL 167
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Db 146 HGFLSNL 152
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RESULT 71

US-09-808-483-18
; Sequence 18, Application US/09808483
; Patent No. US20020001824A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Ligand-gated anion channels of insects
; FILE REFERENCE: Le A 34 397
; CURRENT APPLICATION NUMBER: US/09/808,483
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: DE 100 136 19.2
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-808-483-18

Query Match 2.5%; Score 7; DB 9; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 PILLMKS 225
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Db 411 PILLMKS 417

RESULT 72

US-10-369-493-1984
; Sequence 1984, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1984
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1984

Query Match 2.5%; Score 7; DB 15; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VANTYVY 37
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Db 47 VANTYVY 53

RESULT 73

US-10-282-122A-54850
; Sequence 54850, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54850
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54850

Query Match 2.5%; Score 7; DB 12; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSQH 161
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Db 248 ESSRSQH 254

RESULT 74

US-10-312-273-227
; Sequence 227, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9

; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 227
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-227

Query Match 2.5%; Score 7; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 ESSRSRGH 161
|||
Db 248 ESSRSRGH 254

RESULT 75
US-10-289-762-189
; Sequence 189, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 189
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-189

Query Match 2.5%; Score 7; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 ESSRSRGH 161
|||
Db 248 ESSRSRGH 254

Search completed: March 23, 2004, 09:29:27
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:15:55 ; Search time 60 Seconds
(without alignments)
1323.264 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281
Sequence: 1 MAMMEVGGPSLGTCTVLV.....NEHLIDMDHRSFGAFLVG 281

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A.Geneseq 29Jan04.*

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2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	281	100.0	281	2	AAW27134 Human Apo
3	281	100.0	281	2	AAW19787 Human Apo
4	281	100.0	281	2	AAW76829 Human TL2
5	281	100.0	281	2	AAW56760 Human TRA
6	281	100.0	281	2	AAW44354 Human AGP
7	281	100.0	281	2	AAW01517 Protein a
8	281	100.0	281	2	AAW27012 Human Apo
9	281	100.0	281	3	AAW81956 Human Apo
10	281	100.0	281	3	AAW24038 Human PRO
11	281	100.0	281	3	AAW08545 Amino aci
12	281	100.0	281	3	AAW28691 Human AGP
13	281	100.0	281	4	AAW50977 Human PRO
14	281	100.0	281	4	AAW67243 Human Apo
15	281	100.0	281	4	AAW11031 Human TNF
16	281	100.0	281	4	AAW48350 Human TL2
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18	281	100.0	281	5	AAW31630 Human TRA
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25	281	100.0	281	6	AAW10205 Human Apo

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51	217	77.2	281	2	AAW27017 Human Apo
52	202	71.9	281	2	AAW27019 Human Apo
53	202	71.9	281	2	AAW27016 Human Apo
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57	187	66.5	253	6	ABU08564 Human Gro
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59	187	66.5	256	6	ABU08565 CMV sig.
60	187	66.5	461	5	AAO17496 Antibody-
61	187	66.5	480	5	AAO17495 Antibody-
62	187	66.5	614	3	AAO17494 Antibody-
63	186	66.2	441	3	AAW28692 FC-huAGP-
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65	180	64.1	281	7	ADB61480 Human Apo
66	180	64.1	281	7	ADB61482 Human Apo
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83	166	59.1	166	3	AAW08274 Amino aci
84	161	57.3	161	4	AAW71985 C-termina
85	161	57.3	161	6	ABW39855 TNF famil
86	161	57.3	161	7	ADC03335 Tumour ne
87	161	57.3	161	7	ADC03335 Tumour ne
88	156	55.5	296	4	ABW84402 TRAIL ami
89	141	50.2	246	5	AAW86309 Fusion co
90	139	49.5	139	2	AAU79598 Human TRA
91	133	43.8	133	2	AAW01518 Polypepti
92	123	43.8	123	6	ABW82204 Chimeric
93	107	38.1	113	5	AAU79600 Human TRA
94	105	37.4	188	5	AAU79599 Human TRA
95	91	32.4	121	3	AAW03752 Human sec
96	90	32.0	173	5	ABW72258 Partial h
97	90	32.0	101	2	AAW19790 Human apo
98	90	32.0	101	2	AAW56761 Human TRA

99 90 32.0 101 4 AA11032 Human TRA
100 90 32.0 101 6 AB08559 Human TNF

ALIGNMENTS

RESULT 1
AAW19777
ID AAW19777 standard; protein; 281 AA.

AC AAW19777;

XX 22-SEP-1997 (first entry)

XX Novel cytokine Apo-2 ligand.

XX Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..281

FT /note= "Claim 4"

FT Region 1..14

FT Protein /label= Cytoplasmic_region

FT /note= "Claim 3"

FT Region 15..40

FT /label= Transmembrane_region

FT Protein 41..281

FT /note= "Claim 2"

FT Region 41..281

FT /label= Extracellular_region

FT Modified-site 109

FT /label= Glycosylation

FT /note= "putative N-linked glycosylation site"

FT Protein 114..281

FT /note= "Claim 1"

XX WO9725428-A1.

XX 17-JUL-1997.

XX 08-JAN-1997; 97WO-US000272.

XX 09-JAN-1996; 96US-00584031.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Chuntharapai A, Kim KJ;

XX WPI; 1997-372867/34.

XX N-PSDB; AAW72796.

XX Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce

XX apoptosis for the treatment of breast and colon cancer.

XX Claim 4; Fig 1a; 72pp; English.

XX A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian

XX cell apoptosis. It is believed to be a member of the tumour necrosis

XX factor cytokine family. Its amino acid sequence was deduced from a cDNA

XX clone (AAW72796) isolated from a human placental cDNA library. Apo-2

XX ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-

XX 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells

XX transformed or transfected with a vector contg. Apo-2 ligand nucleic

XX acid. They can be used to induce apoptosis in mammals and to treat

XX pathological conditions such as cancer (esp. breast or colon cancer) or

XX to raise antibodies useful in diagnostic assays

XX Sequence 281 AA;

XX SQ

Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVIFVTLLQSLCAVAVTVVYFTNELKOMQDKYSKSGIACFLKE 60

DB 1 MAMMEVGGPSLGQTCVLIVIFVTLLQSLCAVAVTVVYFTNELKOMQDKYSKSGIACFLKE 60

QY 61 DDSYMDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120

DB 61 DDSYMDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120

QY 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSSESSRSGHSFLNLHLRNGELVIHEKG 180

DB 121 RVAAHITGTRGRSNTLSPNSKNEKALGRKINSSESSRSGHSFLNLHLRNGELVIHEKG 180

QY 181 FYIYSQYIFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKSRNSCKSKDAEYGLY 240

DB 181 FYIYSQYIFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKSRNSCKSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 2

AAW27134

ID AAW27134 standard; protein; 281 AA.

XX AC AAW27134;

XX DT 02-APR-1998 (first entry)

XX DE Human Apoptosis inducing molecule-I (AIM-I).

XX KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;

XX KW tumour necrosis factor ligand superfamily; AIM-I altered expression;

XX KW neoplasia inhibition; anti-inflammatory agent.

XX OS Homo sapiens.

XX PN WO9733899-A1.

XX PD 18-SEP-1997.

XX PF 14-MAR-1996; 96WO-US003773.

XX PR 14-MAR-1996; 96WO-US003773.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM;

XX DR WPI; 1997-470807/43.

XX DR N-PSDB; AAT85210.

XX New isolated apoptosis inducing molecule-I - used to develop products for

XX the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft

XX versus host disease or inflammation.

XX PS Claim 2; Fig 1; 82pp; English.

XX The present sequence represents a human Apoptosis inducing molecule-I

XX (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand

XX superfamily. The products can be used in the diagnosis and treatment of

XX disorders related to under-expression, over-expression or altered

XX expression of AIM-I. AIM-I or agonists can be used for treating

XX autoimmune disorders including systemic lupus erythematosus,

XX immunoproliferative disease lymphadenopathy (lF),

XX angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,

XX diabetes, and multiple sclerosis, graft versus host disease, to inhibit

XX neoplasia such as tumour cell growth, to treat restenosis, to regulate

XX haematopoiesis in endothelial cell development, to stimulate peripheral

CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
 CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
 CC osteoporosis, for preventing graft-host rejection, and as anti-
 CC inflammatory agents, for treating endotoxin shock or to prevent
 CC activation of HIV
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSGGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSGGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQKQISPLVRERGPO 120
 DB 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQKQISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 3
 AAW19787
 ID AAW19787 standard; protein; 281 AA.
 XX
 AC AAW19787;
 XX
 DT 24-SEP-1997 (first entry)
 XX
 DE Human apoptosis inducer cytokine TRAIL.
 XX
 KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
 KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
 KW thrombotic microangioplasty; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..18
 FT Domain /label= Cytoplasmic_domain
 FT Domain 19..38
 FT Domain /label= Transmembrane_domain
 FT Domain 39..281
 FT Domain /label= Extracellular_domain
 FT /note= "contains a receptor-binding region"
 FT Cleavage-site 89..90
 FT /note= "potential KEX2 protease processing site"
 FT Modified-site 109..111
 FT /note= "potential N-glycosylation site"
 FT Cleavage-site 149..150
 FT /note= "potential KEX2 protease processing site"
 XX
 PN WO9701633-A1.
 XX
 XX 16-JAN-1997.
 XX
 XX 25-JUN-1996; 96WO-US010895.
 XX
 XX 29-JUN-1995; 95US-00496632.
 XX 01-NOV-1995; 95US-00548368.
 XX

PA (IMMV) IMMUNEX CORP.
 XX
 PI Wiley SR, Goodwin RG;
 XX
 DR WPI; 1997-118715/11.
 DR N-PSDB; AAT72847.
 XX
 PT TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
 PT cells - useful for treating thrombotic microangiopathy, cancer and viral
 PT infection and for use in assays.
 XX
 PS Claim 10; Page 43-44; 62pp; English.
 XX
 CC Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
 CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
 CC cells, including cancer cells and virally infected cells. Its amino acid
 CC sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in
 CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
 CC polypeptides) can be expressed in host cells and used in the treatment of
 CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
 CC to raise antibodies that may be useful for treating thrombotic
 CC microangiopathies
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSGGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAATVYVFTNELKQMDKYSGGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQKQISPLVRERGPO 120
 DB 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQKQISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYPPDILLMKSARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 4
 AAW76829
 ID AAW76829 standard; protein; 281 AA.
 XX
 AC AAW76829;
 XX
 DT 25-JAN-1999 (first entry)
 XX
 DE Human TL2 protein.
 XX
 KW TR6; tumour necrosis factor related receptor; human; treatment; stroke;
 KW inflammation; arthritis; septicemia; autoimmune disease; restenosis;
 KW transplant rejection; infection; ischaemia; brain injury; bone disease;
 KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;
 KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
 KW TL2; tumour necrosis factor-related apoptosis-inducing ligand.
 XX
 OS Homo sapiens.
 XX
 PN EP870827-A2.
 XX
 PD 14-OCT-1998.
 XX

PF	23-DEC-1997;	97EP-00310562.	Domain	1..18	/note= "N-terminal cytoplasmic domain"
XX	14-MAR-1997;	97US-0041230P.	Region	19..38	/note= "transmembrane region"
PR	09-MAY-1997;	97US-00853684.	Domain	39..281	/note= "extracellular domain"
PR	22-AUG-1997;	97US-00916625.			
XX	(SMIX) SMITHKLINE BEECHAM CORP.				
PA	Deen KC, Young PR;		US5763223-A.		
PI	XX		09-JUN-1998.		
XX	XX		25-JUN-1996;	96US-00670354.	
XX	WPI; 1998-523156/45.		29-JUN-1995;	95US-00496632.	
DR	N-PSDB; AAV63096.		01-NOV-1995;	95US-00548368.	
XX	DNA encoding tumour necrosis factor receptor TR6 - and corresponding		(IMMV) IMMUNEX CORP.		
PT	polypeptide, antibody, agonist, antagonist, etc.		Goodwin RG, Wiley SR;		
PS	Disclosure; Page 32-33; 34pp; English.		XX		
XX	This sequence represents the human tumour necrosis factor (TNF)-related		XX		
CC	receptor, TL2 (also known as tumour necrosis factor-related apoptosis-		XX		
CC	inducing ligand, TRAIL). This protein is used in a method resulting in		XX		
CC	the isolation of the novel human TNF related receptor, TR6. TR6		XX		
CC	polypeptides and polynucleotides can be used in the treatment of chronic		XX		
CC	and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.		XX		
CC	inflammatory bowel disease, psoriasis), transplant rejection, graft vs.		XX		
CC	host disease, infection, stroke, ischaemia, acute respiratory disease		XX		
CC	syndrome, restenosis, brain injury, (acquired autoimmune disease		XX		
CC	syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative		XX		
CC	disorders), atherosclerosis and Alzheimers disease		XX		
XX	Sequence 281 AA;		XX		
SQ	Query Match 100.0%; Score 281; DB 2; Length 281;		XX		
	Best Local Similarity 100.0%; Pred. No. 1.8e-266;		XX		
	Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX		
QY	1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60		XX		
Db	1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMDKYKSGIACFLKE 60		XX		
QY	61 DDSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120		XX		
Db	61 DDSYWDPNDEESMNSPCQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120		XX		
QY	121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEKG 180		XX		
Db	121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLNLHRLNGELVTHEKG 180		XX		
QY	181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNCSKDAEYGLY 240		XX		
Db	181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYVDPDILLMKSARNCSKDAEYGLY 240		XX		
QY	241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281		XX		
Db	241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281		XX		
RESULT 5			XX		
AAW56760			XX		
ID	AAW56760 standard; protein; 281 AA.		XX		
XX	AAW56760;		XX		
AC	05-AUG-1998 (first entry)		XX		
XX	Human TRAIL polypeptide.		XX		
DT	Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;		XX		
XX	Cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.		XX		
XX	Homo sapiens.		XX		
OS	Key	Location/Qualifiers	XX		
XX			XX		
PH			XX		

```

DE XX Human AGP-1.
KW XX Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
KW XX bone resorption; haematopoietic disease.
OS XX Homo sapiens.
FN XX WO9746686-A2.
PD XX 11-DEC-1997.
XX XX
PF XX 06-JUN-1997; 97MO-US009895.
XX XX
PR XX 07-JUN-1996; 96US-00660562.
XX XX
PA (AMGE-) AMGEN INC.
XX XX
XX XX Johnson MJ, Simonet WS, Danilenko DM;
XX XX WPI; 1998-042194/04.
XX XX DR N-PSDB; AAV15295.
XX XX
PT Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
PT XX useful for treating inflammation, bone resorption and haematopoietic
PT XX diseases.
XX XX
PS Claim 7; Page 36-37; 54pp; English.
XX XX
CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
CC bone resorption. It has the same nucleic acid and amino acid (aa)
CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1.
XX XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-286;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVEVQGPSLGGTQCVLIIVFTVLLQSLCAVAVTYVFTNELKOMQDKYSKGIACFLKE 60
DB 1 MAMVEVQGPSLGGTQCVLIIVFTVLLQSLCAVAVTYVFTNELKOMQDKYSKGIACFLKE 60

QY 61 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVREGPQ 120
DB 61 DDSYWDPNDESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQNI SPLVREGPQ 120

QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDILLMKARNCSWCKDAEYGLY 240
DB 181 FYIYSQTYFRFQEEIKENTKNDKQVQIYKYTSYPPDILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 7

```

AAV01517
ID AAY01517 standard; peptide; 281 AA.
AC AAY01517;
XX
DT 27-MAY-1999 (first entry)
XX
DE Protein associated with neurodegenerative and autoimmune diseases.
XX
XX Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX
OS Homo sapiens.
XX
PN FR2766713-A1.
XX
PD 05-FEB-1999.
XX
PF 04-AUG-1997; 97FR-00010176.
XX
PR 04-AUG-1997; 97FR-00010176.
XX
PA (INMR) BIO MERIEUX.
XX
XX Rieger F, Belliveau JF, Perron H;
XX WPI; 1999-156177/14.
XX
XX Use of polypeptide derived from TRAIL protein for diagnosis of
FT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.
XX
PS Claim 2; Page 13; 21pp; French.
XX
XX The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part of the present sequence to produce a
CC diagnostic, prophylactic or therapeutic composition useful in cases of
CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
CC be used in treatment of neurodegenerative disease, lupus erythematosus,
CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
CC nervous system cells, antigenic and specifically recognise the surface
CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex
XX
SQ Sequence 281 AA;

RESULT 8
AA27012
ID AAY27012 standard; protein; 281 AA.
XX AC AAY27012;
XX DT 24-SEP-1999 (first entry)
XX DE Human Apo-2 ligand (Apo-2L) polypeptide.
XX KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
XX KW lupus; immune-mediated glomerular nephritis; human.
XX OS Homo sapiens.
XX FN WO9936535-A1.
XX PD 22-JUL-1999.
XX PF 15-JAN-1999; 99WO-US001039.
XX PR 15-JAN-1998; 98US-00007886.
XX PR 15-APR-1998; 98US-00060533.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
XX DR WPI; 1999-444397/37.
XX DR N-PSDB; AAX86987.
XX PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX PT in mammalian cancer cells.
XX PS Claim 1; Fig 1A; 86pp; English.
XX CC This sequence represents a novel human cytokine, designated Apo-2 ligand
XX CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
XX CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
XX CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
XX CC induce apoptosis for pathological conditions characterized by decreased
XX CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
XX CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
XX CC coding sequence can also be used in quantitative and screening diagnostic
XX CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
XX CC associated with increased apoptosis
XX CC Sequence 281 AA;
Query Match 100.0%; Score 281; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
DB 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
RESULT 9
AAY81956
ID AAY81956 standard; protein; 281 AA.
XX AC AAY81956;
XX DT 10-JUL-2000 (first entry)
XX DE Human Apo-2 ligand protein sequence.
XX KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
XX KW therapy; apoptosis; cancer.
XX OS Homo sapiens.
XX FN US6046048-A.
XX PD 04-APR-2000.
XX PF 08-JAN-1997; 97US-00780496.
XX PR 09-JAN-1996; 96US-0009755P.
XX PA (GETH) GENENTECH INC.
XX PI Kim KJ, Ashkenazi AJ, Chuntharapai A;
XX DR WPI; 2000-282690/24.
XX DR N-PSDB; AAA07425.
XX PT New isolated monoclonal antibodies having antigen specificity for Apo-2
XX PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo
XX PT -2 ligand serum, and for treating diseases associated with increased
XX PT apoptosis.
XX PS Claim 9; Fig 1a; 46pp; English.
XX CC This sequence is the human Apo-2 ligand protein, which is recognised by
XX CC monoclonal antibodies produced by the hybridoma cell lines of the
XX CC invention. The hybridoma cell lines are deposited under the American Type
XX CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
XX CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
XX CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
XX CC tissues, or serum. The antibodies may also be employed as therapeutics.
XX CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
XX CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
XX CC pathological conditions or diseases associated with increased apoptosis.
XX CC They are also useful for the affinity purification of Apo-2 ligand from
XX CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
XX CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
XX CC Sequence 281 AA;
Query Match 100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACFLKE 60
QY 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
DB 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240

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Db      181  FYYYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
      241  SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
Db      241  SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 10
AAB24038
ID      AAB24038 standard; protein; 281 AA.
XX
AC      AAB24038;
XX
DT      25-JAN-2001 (first entry)
XX
DE      Human PRO1096 protein sequence SEQ ID NO:51.
XX
KW      Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KW      identification; tumorigenesis; anticancer; detection.
XX
OS      Homo sapiens.
XX
PN      WO200053750-A1.
XX
PD      14-SEP-2000.
XX
PF      02-DEC-1999; 99WO-US028551.
XX
PR      08-MAR-1999; 99WO-US005028.
PR      01-SEP-1999; 99WO-US020111.
PR      29-OCT-1999; 99US-0162506P.
PR      30-NOV-1999; 99WO-US028313.
PR      01-DEC-1999; 99WO-US028634.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX
DR      WPI; 2000-594320/56.
XX
DR      N-PSDB; AAC58120.
XX
PT      Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT      the growth of tumors in mammals, and to identify inhibitors of PRO
PT      polypeptide activity or expression.
XX
PS      Claim 61; Fig 36; 226pp; English.
XX
CC      The present invention describes an antibody that binds to a human protein
CC      (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
CC      PRO1927; PRO3567; PRO1295; PRO1303; PRO1303; PRO4344; PRO4354; PRO4397;
CC      PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
CC      activity and can be used to diagnose tumours in mammals, by detecting
CC      complex formation when the antibody is contacted with test cells.
CC      Increased expression of genes encoding (I) can also be detected to
CC      diagnose tumours. Agents which inhibit the activity of (I), especially
CC      the antibodies, or an antisense oligonucleotide which hybridises to genes
CC      encoding (I), can be used to inhibit tumour growth, preferably by
CC      inducing cell death. Methods from the present invention can be used to
CC      identify compounds which inhibit the biological activity of (I). AAC58019
CC      to AAC58102 represent PCR primers and hybridisation probes used in
CC      examples from the present invention for human PRO sequences. AAC58103 to
CC      AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
CC      protein sequences given in the exemplification of the present invention
XX
SQ      Sequence 281 AA;

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  MAMMEVOGGSIGQTCVLIVFTVLQSLCAVTVYVFTNELKQMDKYKSGIACFLKE 60
      61  DDSYWDPNDEESMNSPCWQVKQLRQLVRXVILRTSEETISTVQEKQONISPLVRRGPQ 120
      61  DDSYWDPNDEESMNSPCWQVKQLRQLVRXVILRTSEETISTVQEKQONISPLVRRGPQ 120
      121  RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHKG 180
      121  RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHKG 180
      181  FYYYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
      181  FYYYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
      241  SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281
      241  SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLVG 281

RESULT 11
AAB08545
ID      AAB08545 standard; protein; 281 AA.
XX
AC      AAB08545;
XX
DT      20-DEC-2000 (first entry)
XX
DE      Amino acid sequence of a human TRAIL polypeptide.
XX
KW      Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
KW      TNF related apoptosis-inducing ligand; tumour cell;
KW      TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
KW      non-small cell lung carcinoma.
XX
OS      Homo sapiens.
XX
PN      WO200048619-A1.
XX
PD      24-AUG-2000.
XX
PF      15-FEB-2000; 2000WO-US003891.
XX
PR      16-FEB-1999; 99US-0120313P.
XX
PA      (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI      Rosen GD;
XX
DR      WPI; 2000-558253/51.
DR      N-PSDB; AAA64325.
XX
PT      Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
PT      administration of synergistic combination of diterpenoid diepoxide and
PT      tumor necrosis factor related apoptosis-inducing ligand.
XX
PS      Disclosure; Page 23-24; 29pp; English.
XX
CC      The present sequence represents a human TRAIL (tumour necrosis factor
CC      (TNF) related apoptosis-inducing ligand) polypeptide. The specification
CC      describes a method for enhanced killing of tumour cells. The method
CC      comprises contacting a susceptible tumour cell with a synergistic mixture
CC      of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
CC      dosage to kill at least 50 % of the cells. This mixture is synergistic,
CC      and so is active at lower doses and against otherwise resistant cell
CC      lines. The method is used for killing tumour cells, especially solid
CC      tumours or carcinomas (especially mammary carcinoma or non-small cell
CC      lung carcinoma)
XX
SQ      Sequence 281 AA;

Query Match      100.0%; Score 281; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCVAVTYYVFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCVAVTYYVFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
 Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLRNGELVIHEKG 180
 Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12

AAB28691
 ID AAB28691 standard; protein; 281 AA.

XX AAB28691;

DT 14-FEB-2001 (first entry)

DE Human AGP-1.

XX Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
 anti-inflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
 human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 transplant rejection; cardiovascular disease; arteriosclerosis.

XX Homo sapiens.

XX WO200063253-A1.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008004.

XX 16-APR-1999; 99US-00293245.

XX (AMGE-) AMGEN INC.

XX Hsu H, Meng S;

XX WPI; 2000-665240/64.

XX N-PSDE; AAC67831.

XX Fusion protein of AGP-1 protein and an Fc region, used to treat
 proliferative disorders, immune disorders, and virally-induced disorders.

XX Claim 3; Fig 2; 93pp; English.

XX The present sequence is human AGP-1, a type II transmembrane protein.
 XX Fusion proteins comprising an Fc immunoglobulin region fused to the N-
 XX terminal portion of the AGP-1 protein have been produced. The fusion
 XX proteins can be used to induce apoptosis in a tissue, and to treat
 XX proliferative disorders, immune disorders, or virally-induced disorders.
 XX The proliferative disorders include cancers, such as breast, prostate,
 XX lung or colon cancer. The viral infections include hepatitis, and
 XX acquired immunodeficiency syndrome (AIDS), and the immune disorders may
 XX be autoimmune disorders or transplant rejection. Cardiovascular diseases
 XX such as arteriosclerosis may also be treated. The AGP-1 containing fusion
 XX proteins have increased biological activity compared to the soluble AGP-1
 XX proteins used in prior art therapies

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCVAVTYYVFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLQGTCLVIVFTVLLQSLCVAVTYYVFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
 Db 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQNI SPLVRERGQ 120
 QY 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLRNGELVIHEKG 180
 Db 121 RVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSPFLNHLRNGELVIHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYPPDPILLMKARNCSWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13

AAB50977

ID AAB50977 standard; protein; 281 AA.

XX AAB50977;

XX 21-MAR-2001 (first entry)

XX Human PRO1096 protein.

XX Human; PRO; cytostatic; neutropic; neuroprotective; respiratory general;
 XX anti-inflammatory; angiogenic; immunosuppressive; immunostimulant;
 XX PRO agonist; cancer; inflammatory disorder; immunological disorder.

XX Homo sapiens.

XX WO200073348-A2.

XX 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-1999; 99WO-US012252.

XX 22-JUN-1999; 99US-0140650P.

XX 23-JUN-1999; 99US-0141037E.

XX 20-JUL-1999; 99US-0144758P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 29-OCT-1999; 99US-0162506P.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 09-DEC-1999; 99US-0170262P.

XX 16-DEC-1999; 99WO-US030099.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 18-MAR-2000; 2000WO-US006319.

XX 30-MAR-2000; 2000WO-US006884.

XX 17-MAY-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

PA (GETH) GENENTECH INC.
 XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX WPI; 2001-016509/02.
 DR N-PSDB; AAC91579.
 XX
 XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for
 PT treating various tumors, e.g. breast cancer, and other inflammatory,
 PT angiogenic and immunological disorders.
 XX
 XX Claim 31; Fig 54; 188pp; English.
 XX
 XX The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumors, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoeleic disorders, and inflammatory, angiogenic and immunological
 CC disorders
 XX
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDNDDESMNSPCQVQWQVLQVLRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 DB 61 DDSYWDNDDESMNSPCQVQWQVLQVLRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOEIKENTKDKQVYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKDKQVYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14
 AAB67243
 ID AAB67243 standard; protein; 281 AA.
 XX
 XX AAB67243;
 AC
 XX 18-APR-2001 (first entry)
 DT
 XX Human Apo2 ligand.
 DE
 XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.
 KW
 XX Homo sapiens.
 OS
 XX WO2001008332-A1.
 PN
 XX 04-JAN-2001.
 PD
 XX 26-JUN-2000; 2000WO-US017579.
 PF
 XX 28-JUN-1999; 99US-0141342P.
 PR

XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
 PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
 XX WPI; 2001-123012/13.
 DR
 XX
 XX Use of divalent metal ions for making Apo-2 ligand and in formulations
 PT containing Apo-2 ligand for increasing yield and stability of ligand
 PT trimers, useful for therapeutic applications.
 XX
 XX Claim 6; Fig 1; 60pp; English.
 XX
 XX The present invention relates to a formulation comprising Apo-2 ligand
 CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
 CC treating cancers and viral infections. Addition of divalent metal ions
 CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
 CC in increased yield and stability of Apo-2 ligand trimers
 XX
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIIVFTVLLQSLCAVAVTVYVFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDNDDESMNSPCQVQWQVLQVLRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 DB 61 DDSYWDNDDESMNSPCQVQWQVLQVLRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 QY 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 DB 121 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 QY 181 FYIYSQTYFRFOEIKENTKDKQVYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKDKQVYIYKYTSYDPDILLMKSARNCSWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 15
 AAEL1031
 ID AAEL1031 standard; protein; 281 AA.
 XX
 XX AAEL1031;
 AC
 XX 18-DEC-2001 (first entry)
 DT
 XX Human TNF related apoptosis inducing ligand (TRAIL) protein.
 DE
 XX Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 KW melanoma.
 XX
 XX Homo sapiens.
 OS
 XX Key
 FH Location/Qualifiers
 FT 1. 18
 FT /label= N_terminal_cytoplasmic_domain
 FT 19-38
 FT /label= Transmembrane_region
 FT 39..281
 FT /label= Extracellular_domain
 XX
 XX US6284236-B1.

XX 04-SEP-2001.
 XX 26-MAY-1999; 99US-00320424.
 XX 29-JUN-1995; 95US-00496632.
 XX 01-NOV-1995; 95US-00548368.
 XX 25-JUN-1996; 96US-00670354.
 XX 26-MAR-1998; 98US-00048641.
 XX 10-NOV-1998; 98US-00190046.
 XX (IMMV) IMMUNEX CORP.
 XX Wiley SR, Goodwin RG;
 XX WPI; 2001-595463/67.
 XX N-PSDB; AAD18395.
 XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
 XX for treating viral infections (e.g. bovine viral diarrhoea or human
 XX immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
 XX Claim 2; Col 45-48; 41pp; English.
 XX The invention relates to a cytokine designated as tumour necrosis factor
 XX (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
 XX of certain target cells, including cancer cells and virally infected
 XX cells. The TRAIL polypeptides are useful in killing cancer cells, in
 XX treating viral infections (e.g. bovine viral diarrhoea or human
 XX immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
 XX melanoma), as a research reagent useful in studying apoptosis including
 XX the regulation of programmed cell death. TRAIL DNA sequences may be
 XX employed in developing a gene therapy approach to treating disorders
 XX mediated by defective or insufficient amounts of TRAIL, in the production
 XX of TRAIL polypeptides and as probes or primers in polymerase chain
 XX reactions (PCR). The present sequence is human TRAIL protein
 XX SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQEEIKENTKNDQVQYIKYTSYDPDILLMKSAKNSCKDAEYGLY 240
 Db 181 FYIYISQTYFRFQEEIKENTKNDQVQYIKYTSYDPDILLMKSAKNSCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 16
 AAB48350
 ID AAB48350 standard; protein; 281 AA.
 XX
 AC AAB48350;
 XX
 XX 20-APR-2001 (first entry)
 XX Human TL2 polypeptide.

XX Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
 KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;
 KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;
 KW neutropic; neuroprotective; antiarthritic; antirheumatic; antileukemic;
 XX gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
 OS Homo sapiens.
 XX WO2000077191-A1.
 XX 21-DEC-2000.
 XX 12-JUN-2000; 2000WO-US016134.
 XX 15-JUN-1999; 99US-00333593.
 XX (SMIX) SMITHLINE BEECHAM CORP.
 XX Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
 XX WPI; 2001-112223/12.
 XX N-PSDB; AAC84745.
 XX New tumor necrosis factor related receptor TR6 polynucleotides and
 XX polypeptides useful for e.g. for treating chronic and acute inflammation,
 XX arthritis, septicemia, autoimmune diseases, infection, cancer, bone
 XX diseases.
 XX Disclosure; Page 26; 47pp; English.
 XX The invention relates to a human tumour necrosis factor (TNF) related
 XX receptor, TR6. TR6 can be expressed by standard recombinant methodology.
 XX The TR6 polypeptides are useful for treating chronic and acute
 XX inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
 XX inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
 XX host disease, infection, stroke, ischaemia, acute respiratory disease
 XX syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
 XX atherosclerosis, and Alzheimer's disease. These may also be used to
 XX inhibit production of TNF-alpha and eicosanoids, as research reagents and
 XX materials for discovering treatments and diagnostics to animal and human
 XX diseases. The polypeptides may further be used as immunogens to produce
 XX antibodies immunospecific for the TR6 polypeptides. The polynucleotides
 XX may also be used as hybridization probes for cDNA and genomic DNA for
 XX isolating full-length cDNAs and genomic clones encoding TR6 and of other
 XX genes having high sequence similarity to TR6 gene, and for chromosome
 XX identification. The present sequence represents a human TL2 polypeptide.
 XX TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
 XX a ligand for the TL2 polypeptide
 XX SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 Db 61 DDSYWDNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQEEIKENTKNDQVQYIKYTSYDPDILLMKSAKNSCKDAEYGLY 240
 Db 181 FYIYISQTYFRFQEEIKENTKNDQVQYIKYTSYDPDILLMKSAKNSCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

```

Db      241 SIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
|||||
RESULT 17
ABB08133
ID ABB08133 standard; protein; 281 AA.
XX
AC ABB08133;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protoacide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200236141-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US044834.
XX
PR 02-NOV-2000; 2000US-0245721P.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
PI Thomas EK;
XX
DR WPI; 2002-500114/53.
XX
PT Treating an individual suffering from infection, e.g. inflammation,
PT chickenpox or AIDS, by administering a combination of dendritic cell
PT mobilization factor or maturation agent, T cell enhancing factor and
PT antigen-specific T cells.
XX
PS Disclosure; Page 40-42; 43pp; English.
XX
CC The invention relates to treating an individual at risk for or suffering
CC from infection with a pathogenic or opportunistic organism. The method
CC involves administering a combination of two to five agents comprising:
CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
CC agent; (c) dendritic cell activation factor; (d) T cell enhancing factor;
CC or (e) activated, antigen-specific T cells. The methods are useful for
CC treating an individual at risk for or suffering from infection with a
CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
CC T. cruzi, which causes Chaga's disease). The methods are especially
CC useful for treating an individual suffering from immunosuppression by
CC enhancing a lymphocyte-mediated immune response. In particular, the
CC method is useful for treating inflammations, chickenpox, oral or genital
CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
CC cell leukemia or T cell lymphoma. The activated antigen-presenting
CC dendritic cells are useful as a vaccine adjuvant. The present sequence
CC represents a human TRAIL polypeptide fragment
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
QY 61 DSDYWDPNDESMNSPCQVQKWLRLVRLKMLRTSEETISTVQEKQNI SPLVRGPG 120
Db 61 DSDYWDPNDESMNSPCQVQKWLRLVRLKMLRTSEETISTVQEKQNI SPLVRGPG 120

```

```

QY 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
Db 121 RVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
QY 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMSARNSCWSKDAEYGLY 240
Db 181 FYYIYSQTYFRFQBEIKENTKNDKQVQYIYKYTSYDPDILLMSARNSCWSKDAEYGLY 240
QY 241 SIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGIPELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

```

```

RESULT 18
ABG31630
ID ABG31630 standard; protein; 281 AA.
XX
AC ABG31630;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human TRAIL protein.
XX
KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;
KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;
KW dendritic cell activator; T cell enhancer; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200266044-A2.
XX
PD 29-AUG-2002.
XX
PF 23-OCT-2001; 2001WO-US046254.
XX
PR 24-OCT-2000; 2000US-0242868P.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
XX WPI; 2002-674891/72.
XX
PT Treating an individual with tumors or cancers, e.g. liver cancer or brain
PT tumor, by administering a combination of dendritic cell populations, T
PT cell enhancing factors and activated, antigen-specific T cells.
XX
PS Disclosure; Page 41-43; 44pp; English.
XX
CC The present invention relates to a new method for treating a tumour-
CC bearing subject. The method involves administering a combination of 2 to
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
CC maturation agent, tumour-killing agent, T cell enhancing factor or
CC activated, antigen-specific T cells. The method is useful for treating
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
CC cervical intraepithelial neoplasia. The present amino acid sequence
CC represents the human TRAIL protein that was used in the method of the
CC invention
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVTVYVFTNELKQMDKYSGIACFLKE 60

```

QY 61 DDSYDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGPQ 120
 Dd 61 DDSYDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 Dd 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 QY 181 FYYISQTYFRFOEBIKENTKNDKQVQYIKYTSYPPDPILLMKSARNCSWCKDAEYGLY 240
 Dd 181 FYYISQTYFRFOEBIKENTKNDKQVQYIKYTSYPPDPILLMKSARNCSWCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 Dd 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281

RESULT 19

AAU75062 ID AAU75062 standard; protein; 281 AA.
 AC AAU75062;
 XX
 XX 23-APR-2002 (first entry)
 XX
 XX Human TNF related apoptosis inducing ligand (TRAIL) protein.
 XX TRAIL; TNF; apoptosis; tumour; death domain receptor ligand;
 KW diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma;
 KW mammary adenocarcinoma; non-small cell lung carcinoma;
 KW neurological malignancy; haematological malignancy; lichen planus;
 KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
 KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
 KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
 KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
 KW discoid lupus erythematosus; human.
 XX
 XX Homo sapiens.
 OS
 XX US6329148-B1.
 XX
 XX 11-DEC-2001.
 XX
 XX 15-FEB-2000; 2000US-00505250.
 XX
 XX 16-FEB-1999; 99US-0120313P.
 XX 20-AUG-1999; 99US-0149989P.
 XX
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Rosen GD, Kao P;
 PI
 XX WPI; 2002-121125/16.
 DR N-PSDB; ABK13192.
 XX
 XX Use of a synergistic combination of death domain receptor ligands and
 PT diterpenoid triepoxides for killing of tumor cells.
 XX
 XX Disclosure; Col 17-20; 20pp; English.
 XX
 XX This invention relates to a novel method for enhanced killing of tumour
 CC cells comprising contacting a tumour cell with a synergistic combination
 CC of a death domain receptor ligand and a diterpenoid triepoxide. This
 CC method has cytostatic activity and works by blocking TNF-alpha mediated
 CC induction of c-IAP2 and c-IAP1. The method of the invention may be used
 CC for treating tumours, particularly solid tumours, e.g. carcinoma, mammary
 CC adenocarcinoma and non-small cell lung carcinoma also neurological
 CC malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma,
 CC chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis
 CC fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-
 CC cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid
 CC lupus erythematosus, lichen planus. The combination may be administered

CC with other active agents, e.g. anti- metastatic, anti-tumour or anti-
 CC angiogenic agents. The potent synergy between the diterpenoids and the
 CC death domain ligands allows increased killing at equivalent or lower
 CC doses, and can sensitize otherwise resistant cells. This sequence
 CC represents the human TNF related apoptosis inducing ligand (TRAIL)
 CC protein sequence. TRAIL is a death domain receptor used in the used
 CC method of the invention in combination with diterpenoid triepoxides to
 CC kill tumours by induction of apoptosis
 XX
 QY Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60
 Dd 1 MAMMEVQGGPSLGQTCVLIVITVLLQSLCVAVTVVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DDSYDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGPQ 120
 Dd 61 DDSYDPNDESMNSPCWQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGRGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 Dd 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 QY 181 FYYISQTYFRFOEBIKENTKNDKQVQYIKYTSYPPDPILLMKSARNCSWCKDAEYGLY 240
 Dd 181 FYYISQTYFRFOEBIKENTKNDKQVQYIKYTSYPPDPILLMKSARNCSWCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 Dd 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVNG 281
 RESULT 20
 AAMS1077 ID AAMS1077 standard; protein; 281 AA.
 XX
 AC AAMS1077;
 XX
 XX 30-MAY-2002 (first entry)
 DT
 XX Human Apo-2 ligand (TRAIL).
 DE
 XX Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour;
 KW antitumour; therapy.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Protein 114..281
 FT /note= "Apo-2L polypeptide used in method of Claim 18"
 FT
 XX WO200209755-A2.
 PN
 XX 07-FEB-2002.
 PD
 XX
 XX 27-JUL-2001; 2001WO-US023691.
 PF
 XX 27-JUL-2000; 2000US-0221256P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Escandon E, Fox JA, Kelley SK, Xiang H;
 PI WPI; 2002-268997/31.
 XX
 XX Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I
 PT inhibitor class, and Apo-2 ligand receptor agonist for enhancing
 PT apoptosis in mammalian cells, or for treating cancer in a mammal.
 XX

PS Claim 18; Page 79-80; 84pp; English.

XX The present sequence is that of human Apo-2L ligand (Apo-2L or TRAIL). The

CC invention relates to methods of inducing apoptosis in mammalian cells,

CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a

CC chemotherapeutic agent of the topoisomerase I inhibitor class) to

CC synergistically induce apoptosis in mammalian cells, in particular

CC mammalian cancer cells, and especially colorectal cancer cells (claimed).

CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering

CC from cancer or a condition in which induction of apoptosis in the cells

CC is desirable. A claimed method of treating cancer in a mammal comprises

CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is

CC administered about 6-72 hours prior to administration of the Apo-2L

CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L

CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or

CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and

CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,

CC directing the cells towards an apoptotic pathway rather than cell cycle

CC arrest and possible DNA repair, thus providing enhanced antitumour

CC activity. An example illustrates the synergistic inhibition of tumour

CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human

CC COLO205 colon carcinoma cells

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.8e-266;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120

DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

QY 181 FYIYSOTYFRFQEEIKENTKNDKQVQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240

DB 181 FYIYSOTYFRFQEEIKENTKNDKQVQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 21

ABP51954

ID ABP51954 standard; protein; 281 AA.

XX

AC ABP51954;

XX

DT 09-OCT-2002 (first entry)

XX

XX Human Apo-2 ligand protein sequence SEQ ID NO:4.

DE Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;

XX humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;

KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;

KW anti-CD11a; Fab; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab';

XX anti-VEGF Fab.

OS Homo sapiens.

XX

XX WO200248376-A2.

PN

XX 20-JUN-2002.

PD

XX 07-DEC-2001; 2001WO-US047581.

XX

PR 14-DEC-2000; 2000US-0256162P.

XX (GETH) GENENTECH INC.

PA Chen CY;

XX

PI WPI; 2002-583522/62.

XX

DR N-PSDB; ABQ73920.

XX

PT Novel Escherichia coli strain useful for producing polypeptide, deficient

PT in degP and prc encoding protease, and harboring mutant spr gene, product

PT of gene suppresses growth phenotypes of strains harboring prc mutants.

XX

XX Example 1; Fig 4; 63pp; English.

PS The present invention describes an Escherichia coli strain (I) deficient

CC in chromosomal degP and prc encoding protease DegP and Prc, respectively,

CC and harbouring a mutant spr gene, the product of mutant spr gene

CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.

CC (I) is useful for producing a polypeptide, by culturing (I) comprising

CC nucleic acid encoding the polypeptide, which is heterologous to the

CC strain, such that the nucleic acid is expressed, and recovering the

CC heterologous polypeptide from the strain. The heterologous polypeptide is

CC proteolytically sensitive. Culturing of (I) is performed in a fermentor

CC under conditions of high- or low-cell density fermentation. The

CC polypeptide is recovered from the periplasm or culture medium of the

CC strain. The polypeptide is an antibody (humanised or full-length

CC antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular

CC endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,

CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an

CC antibody fragment having a light chain (kappa light chain). The antibody

CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18

CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper

CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-

CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-

CC CD18 Fab'2-leucine zipper fusion with a 6-lysine tag, and anti-CD18

CC Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence

CC represents a human Apo-2 ligand amino acid sequence from the present

CC invention

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;

Best Local Similarity 100.0%; Pred. No. 1.8e-266;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60

DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVYFTNELKQMDKYSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120

DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

DB 121 RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

QY 181 FYIYSOTYFRFQEEIKENTKNDKQVQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240

DB 181 FYIYSOTYFRFQEEIKENTKNDKQVQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 22

AAO19095

ID AAO19095 standard; protein; 281 AA.

XX

XX AAO19095;

AC

XX

```
DT 22-NOV-2002 (first entry)
XX C neoformans antigen expressing dendritic cell related protein #4.
DE Human; fungicide; fungal infection; dendritic cell; antigen;
XX Cryptococcus neoformans; vaccine; immunostimulant.
KW Homo sapiens.
XX WO200266053-A2.
XX 29-AUG-2002.
XX 14-DEC-2001; 2001WO-US048288.
XX 04-JAN-2001; 2001US-0259653P.
XX (IMMV ) IMMUNEX CORP.
XX Thomas EK;
XX WPI; 2002-674896/72.
XX Producing a population of activated, Cryptococcus neoformans antigen-
PT presenting dendritic cells for preventing or treating C. neoformans
PT infection comprises causing the obtained dendritic cells to present the
PT antigen.
XX Disclosure; Page 29-30; 32pp; English.
XX The present invention relates to a method of producing a population of
CC activated, Cryptococcus neoformans antigen-presenting dendritic cells,
CC comprising causing the obtained dendritic cells to present the antigen
CC and maturing the dendritic cells. The activated, C. neoformans antigen-
CC expressing dendritic cells are useful for treating, or as vaccines or
CC vaccine adjuvants against, C. neoformans infection, or for generating
CC antigen-specific T cells. The present sequence is a human protein shown
CC in the exemplification of the invention
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 281; DB 5; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-266;
XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVYFTNELKQMDKYSGIACFLKE 60
QY 61 DSYNDPNDDEESNPSQWQKQQLRVKMLRTSEETSTVQEKQNNISPLVRRGQ 120
DB 61 DSYNDPNDDEESNPSQWQKQQLRVKMLRTSEETSTVQEKQNNISPLVRRGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVHEKG 180
QY 181 FYIYSQTYFRQEEIKENTKDKQKQVQIYKYTSPDPIILMKASRNCSWKDAPYGLY 240
DB 181 FYIYSQTYFRQEEIKENTKDKQKQVQIYKYTSPDPIILMKASRNCSWKDAPYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
XX
XX RESULT 23
XX AAU79593
XX ID AAU79593 standard; protein; 281 AA.
XX AC AAU79593;
XX 24-SEP-2002 (first entry)
DT
```

```
XX Human TNF-related apoptosis inducing ligand (TRAIL) protein.
DE Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
XX tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
XX chromosome 3q26.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 1..16
FT /note= "Cytoplasmic domain"
FT Domain 17..38
FT /note= "Transmembrane domain"
FT Domain 39..281
FT /note= "Extracellular domain"
FT Domain 118..256
FT /note= "TNF domain"
XX
XX US2002061525-A1.
XX 23-MAY-2002.
XX 16-MAY-2001; 2001US-00855544.
XX 16-MAY-2000; 2000IL-00136156.
XX (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
PI Yelin R, Khoeravi R, Savitzky K;
XX WPI; 2002-479259/51.
XX
XX New splice variants of tumor necrosis factor-related apoptosis inducing
PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
PT diseases or disorders associated with low expression of the variants.
XX
XX Disclosure; Fig 9; 29pp; English.
XX The invention discloses isolated, naturally occurring, polypeptide splice
CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing
CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal
CC cellular differentiation and development of multicellular organisms.
CC Apoptosis is induced by certain cytokines which include TNF and TRAIL
CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane
CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in
CC many tissues and cells. Receptors for TRAIL include two death domain
CC containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1
CC and DcR2, lacking the intracellular signalling death domain. TRAIL,
CC induced by type I interferons, induces apoptosis in tumour cells, whereas
CC normal cells are relatively resistant without showing significant toxic
CC side effects. Thus, TRAIL has the potential to be a very useful
CC antitumour agent. The naturally occurring splice variants may differ in
CC their cellular distribution, expression levels/timing and activity.
CC Determining these factors could provide possible mechanisms for the
CC induction of apoptosis of tumours cells. The splice variant polypeptides
CC and polynucleotides can be used in gene therapy, to raise antibodies, to
CC detect the levels, distribution and ratios of expression of TRAIL, and
CC its splice variants, in a biological sample and to identify compounds
CC which bind the variant TRAIL products and modulate its activity (agonists
CC and antagonists). Pharmaceutical compositions, comprising an expression
CC vector or any of the amino acid sequences, are useful for causing a
CC cytotoxic effect in cancer cells and for treatment of diseases which can
CC be ameliorated, cured or prevented by lowering or raising the level of
CC the amino acid sequences. The antibodies may also have a therapeutic
CC utility in blocking or decreasing the activity of the TRAIL variant
CC products. Diseases that may be treated include cancer, neurodegenerative
```

CC diseases, autoimmune diseases, diseases involved in the non-normal
 CC development of tissues and aging. TRAIL's gene is located on chromosome
 CC 3q26. The sequence presented is the wild-type human TNF-related apoptosis
 CC inducing ligand (TRAIL) protein
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGGIACFLKE 60

QY 61 DSDYDNDPNDDESMNCPQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120
 Db 61 DSDYDNDPNDDESMNCPQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKARNCSWCKDAEYGLY 240
 Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 24

ID ABG73861
 AC ABG73861 standard; protein; 281 AA.

XX AC ABG73861;

XX 03-APR-2003 (first entry)

DT Human Apo-2 ligand protein.

DE Human Apo-2 ligand protein.

XX Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
 KW nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS;
 KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;
 KW aplastic anaemia; myocardial infarction; stroke; reperfusion injury;
 KW toxin-induced liver disease; cancer; lupus; herpes virus infection.

XX Homo sapiens.

XX Key

FH Location/Qualifiers

FT 15..40

FT Domain /note= "Transmembrane domain"

FT 41..281

FT Domain /note= "Extracellular domain"

FT Modified-site 109

FT /note= "N-glycosylated"

XX US6462176-B1.

XX 08-OCT-2002.

XX 11-SEP-1997; 97US-00928069.

XX 23-SEP-1996; 96US-0026943P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2003-173840/17.

XX DR

DR N-PSDB; ABX15469.

XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
 PT mammalian cells, for generating antibodies, in affinity purification
 PT techniques, and in competitive-type receptor binding assays.
 XX

PS Example 4; Fig 4; 52pp; English.

XX The invention relates to an Apo-3 polypeptide having an extracellular
 CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
 CC has been found to stimulate or induce apoptotic activity in mammalian
 CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
 CC receptor (TNFR) family of polypeptides. The invention also relates to a
 CC chimeric molecule comprising an extracellular domain sequence comprising
 CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
 CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in
 CC mammalian cells. Decreased levels of apoptosis has been associated with
 CC conditions such as cancer, lupus, and herpes virus infection. Increased
 CC levels of apoptosis are associated with diseases such as acquired
 CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
 CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
 CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.
 CC The Apo-3 polypeptide is also useful in non-therapeutic applications such
 CC as in quantitative diagnostic assays as a control against which samples
 CC containing unknown quantities of Apo-3 may be prepared, in generating
 CC antibodies, as standards in assays for Apo-3, in affinity purification
 CC techniques, and in competitive-type receptor binding assays. The chimeric
 CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor
 CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
 CC Apo-3 antibodies. The present sequence represents polypeptide sequence of
 CC the human Apo-2 ligand protein which is also reported to be involved in
 CC apoptotic cell death. In the current invention the apoptotic activity of
 CC the Apo-2 ligand protein was measured on human lymphoid cells

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGGIACFLKE 60

Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGGIACFLKE 60

QY 61 DSDYDNDPNDDESMNCPQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120

Db 61 DSDYDNDPNDDESMNCPQVQKWLQRLVRKMLRTSEETISTVQEKQNISPLVRGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

QY 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKARNCSWCKDAEYGLY 240

Db 181 FYIYSQTYFRFQBEIKENTKNDKQVQYIYKTSYDPDILLMKARNCSWCKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281

RESULT 25

ABU10205

ID ABU10205 standard; protein; 281 AA.

XX AC ABU10205;

XX 11-AUG-2003 (first entry)

XX Human Apo-2 ligand.

XX Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;

XX KW

neurodegenerative disease; immunosuppressive; tissue typing.

XX OS Homo sapiens.
XX PN US2003004313-A1.
XX PD 02-JAN-2003.
XX PF 28-MAR-2002; 2002US-00112193.
XX PR 23-SEP-1996; 96US-0026943P.
XX PR 11-SEP-1997; 97US-00928069.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ;
XX DR WPI; 2003-438872/41.
XX DR N-PSDB; ACA61636.
XX PT New isolated Apo-3 polypeptides, useful for stimulating or inducing
XX PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
XX PS or ex vivo gene therapy techniques.
XX PS Example 4; Fig 4; 50pp; English.
XX CC The invention relates to an isolated Apo-3 polypeptide. The Apo-3
XX CC polypeptides are useful for stimulating or inducing apoptotic activity in
XX CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
XX CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
XX CC apoptosis, or as immunogens used in generating antibodies. The
XX CC antagonistic antibodies may be used to block excessive apoptosis, for
XX CC instance in neurodegenerative disease, or to block potential autoimmune/
XX CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
XX CC nucleic acid sequences are useful as diagnostics for tissue-specific
XX CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
XX CC knockout animals. The transgenic or knockout animals are useful in
XX CC developing and screening of therapeutically useful reagents. The present
XX CC sequence represents the amino acid sequence of human Apo-2 ligand
XX SQ Sequence 281 AA;
Query Match 100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEYQGGPSLGQTCVLIVFTVLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEYQGGPSLGQTCVLIVFTVLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYWDNDPDEESMNSPCWQVKQQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
Db 61 DSYWDNDPDEESMNSPCWQVKQQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWSSRSGHSLNHLRNGELVIHEKG 180
Db 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWSSRSGHSLNHLRNGELVIHEKG 180
QY 181 FYYISQTYFRFQEEIKENTKDKQWQVIYKYTSYDPDILLMKSRNSCWKDAEYGLY 240
Db 181 FYYISQTYFRFQEEIKENTKDKQWQVIYKYTSYDPDILLMKSRNSCWKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 26

ABU71443

ID ABU71443 standard; protein; 281 AA.

XX

AC

XX

09-JUN-2003 (first entry)

XX DE Human neoplasia inhibiting PRO polypeptide PRO1096.
XX KW Human; tumor; cancer; neoplasia; liver cancer; sarcoma; breast cancer;
KW ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW central nervous system cancer; hepatic carcinoma; glioblastoma;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macropaghal disorder;
KW epithelial disorder; stromal disorder; blastocoelic disorder;
KW inflammatory disorder; angiogenic disorder; immunologic disorder.
XX OS Homo sapiens.
XX PN US2002192209-A1.
XX PD 19-DEC-2002.
XX PF 30-NOV-2001; 2001US-00001054.
XX PR 17-SEP-1997; 97US-0059114P.
XX PR 27-MAR-1998; 98US-0073689P.
XX PR 30-MAR-1998; 98US-0079920P.
XX PR 24-APR-1998; 98US-0082999P.
XX PR 29-APR-1998; 98US-0083545P.
XX PR 12-MAY-1998; 98US-0085149P.
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 11-JUN-1998; 98US-0088858P.
XX PR 25-JUN-1998; 98US-0090691P.
XX PR 17-AUG-1998; 98US-0096891P.
XX PR 17-AUG-1998; 98US-0096894P.
XX PR 10-SEP-1998; 98US-0099803P.
XX PR 10-SEP-1998; 98US-0099803P.
XX PR 14-SEP-1998; 98US-0100263P.
XX PR 15-SEP-1998; 98US-0100390P.
XX PR 23-SEP-1998; 98US-0101476P.
XX PR 10-NOV-1998; 98US-0107783P.
XX PR 18-NOV-1998; 98US-0108849P.
XX PR 19-NOV-1998; 98US-0118099P.
XX PR 15-DEC-1998; 98US-0112420P.
XX PR 22-DEC-1998; 98US-0021851P.
XX PR 22-DEC-1998; 98US-0113296P.
XX PR 05-JAN-1999; 99WO-US000106.
XX PR 12-JAN-1999; 99US-0115554P.
XX PR 12-JAN-1999; 99US-0115558P.
XX PR 20-JAN-1999; 99US-0116533P.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1999; 99US-0123618P.
XX PR 12-APR-1999; 99US-00284291.
XX PR 20-APR-1999; 99WO-US008615.
XX PR 27-APR-1999; 99US-0131294P.
XX PR 02-JUN-1999; 99WO-US012952.
XX PR 22-JUN-1999; 99US-0140650P.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 25-AUG-1999; 99US-00380137.
XX PR 25-AUG-1999; 99US-00380138.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 09-SEP-1999; 99US-00380913.
XX PR 18-OCT-1999; 99US-00403297.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 10-NOV-1999; 99US-00423741.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.

18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000US-0187202P.
15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
08-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006866.
09-MAR-2001; 2001US-00802706.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872034.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
14-JUN-2001; 2001US-00882836.
20-JUN-2001; 2001US-00919892.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
13-AUG-2001; 2001US-00929404.
28-AUG-2001; 2001US-00941992.
29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
(GETH) GENENTECH INC.
Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC,
Shelton DL, Smith V, Watanabe CK, Wood WI;
WPI; 2003-328851/06.
N-PSDB; ACA58016.
Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
treating tumor, preferably cancer, or for treating neuronal, glial,
hypothalamic, stromal, inflammatory, angiogenic and immunologic
disorders.
Claim 32; Fig 54; 186pp; English.
The invention relates to an isolated secreted and transmembrane
polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
associated signal peptide or PRO polypeptide extracellular domain with or
without its associated signal peptide. The PRO polypeptide or an antibody
binding to it is useful for inhibiting the growth of a tumor cell. A
composition containing a PRO polypeptide is useful for inhibiting
neoplastic cell growth or for treating a tumor, preferably cancer (such
as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
bladder, gastric, pancreatic, vulval, thyroid, central nervous system
cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
agonists. The PRO polypeptide or an antibody binding to it is useful in
the preparation of a medicament for treating a condition which is
responsive to the PRO polypeptide or an antibody binding to it. The PRO
polypeptide or an antibody binding to it is also useful for treating
neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
epithelial, stromal, blastocoeic, inflammatory, angiogenic and
immunologic disorders. The present sequence represents the amino acid
sequence of a PRO polypeptide of the invention
Sequence 281 AA;
Query Match 100.0%; Score 281; DB 6; Length 281;
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000US-0187202P.
15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
08-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006866.
09-MAR-2001; 2001US-00802706.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872034.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
14-JUN-2001; 2001US-00882836.
20-JUN-2001; 2001US-00919892.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
13-AUG-2001; 2001US-00929404.
28-AUG-2001; 2001US-00941992.
29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
(GETH) GENENTECH INC.
Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC,
Shelton DL, Smith V, Watanabe CK, Wood WI;
WPI; 2003-328851/06.
N-PSDB; ACA58016.
Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
treating tumor, preferably cancer, or for treating neuronal, glial,
hypothalamic, stromal, inflammatory, angiogenic and immunologic
disorders.
Claim 32; Fig 54; 186pp; English.
The invention relates to an isolated secreted and transmembrane
polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
associated signal peptide or PRO polypeptide extracellular domain with or
without its associated signal peptide. The PRO polypeptide or an antibody
binding to it is useful for inhibiting the growth of a tumor cell. A
composition containing a PRO polypeptide is useful for inhibiting
neoplastic cell growth or for treating a tumor, preferably cancer (such
as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
bladder, gastric, pancreatic, vulval, thyroid, central nervous system
cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
agonists. The PRO polypeptide or an antibody binding to it is useful in
the preparation of a medicament for treating a condition which is
responsive to the PRO polypeptide or an antibody binding to it. The PRO
polypeptide or an antibody binding to it is also useful for treating
neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
epithelial, stromal, blastocoeic, inflammatory, angiogenic and
immunologic disorders. The present sequence represents the amino acid
sequence of a PRO polypeptide of the invention
Sequence 281 AA;
Query Match 100.0%; Score 281; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACFLKE 60
Qy 61 DDSYWDNDDEESNPSQWQVQKQWLQRLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
Db 61 DDSYWDNDDEESNPSQWQVQKQWLQRLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHG 180
Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSARNCSWCKDAEYGLY 240
Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
RESULT 27
ABG72738
ID ABG72738 standard; protein; 281 AA.
XX
AC ABG72738;
XX
DT 17-FEB-2003 (first entry)
XX
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
XX
KW Human; allergic disease; allergy; TNF; TRAIL; diagnosis;
KW tumour necrosis factor-related apoptosis inducing ligand;
KW atopic skin inflammation.
OS Homo sapiens.
XX
PN WO200283946-A1.
XX
PD 24-OCT-2002.
XX
PF 01-MAR-2002; 2002WO-JP001914.
XX
PR 06-APR-2001; 2001JP-00108631.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
XX
PI Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
XX
XX
DR WPI; 2003-093037/08.
DR N-PSDB; ABX13715.
XX
PT Measurement of the expression level of TNF related apoptosis inducing
PT ligand gene for diagnosis and examination of allergic disease and
PT screening agents for allergic disease treatment.
XX
PS Disclosure; Page 51-52; 58pp; Japanese.
XX
CC The invention discloses a method for examining allergic diseases, which
CC comprises measuring the expression level of tumour necrosis factor (TNF)-
CC related apoptosis inducing ligand (TRAIL) gene in a specimen from the
CC patient and comparing this level with the level in healthy persons. TRAIL
CC gene expression is decreased in patients. The nucleic acids and
CC polypeptide can be used to screen for agents for the treatment of
CC allergic diseases, possibly using a transgenic rodent as a model animal
CC for the disease, with effectiveness determined by changes in expression
CC levels or protein activity. The method is useful for the diagnosis,
CC examination, prevention and treatment of allergic diseases, including
CC atopic skin inflammation. The sequence presented is the human TRAIL

CC protein
 XX Sequence 281 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 281; DB 6; Length 281;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNKLQMDKYSGKIACFLKE 60
 DB 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNKLQMDKYSGKIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRVLKMLRTSEETISTVQKQKQNISPLVREGPQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRVLKMLRTSEETISTVQKQKQNISPLVREGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAKNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAKNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 28
 AAO29543
 ID AAO29543 standard; protein; 281 AA.
 AC AAO29543;
 DT 27-AUG-2003 (first entry)
 DE Human TRAIL protein.
 XX

Human; TNF-related apoptosis-inducing ligand; Kaposi's sarcoma; cancer;
 hyperproliferative disorder; rheumatoid arthritis; Parkinson's disease;
 neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease;
 allergic disorder; acquired immune deficiency syndrome; ocular disorder;
 myasthenia gravis; autoimmune disorder; Huntington's disease; vaccine;
 septic shock; multiple sclerosis; inflammatory disorder; liver injury;
 infectious diseases; myelodysplastic syndrome; cardiovascular disorder;
 graft-versus-host disease; toxin-induced liver disease; cachexia; AIDS;
 cerebrovascular disorder; thrombotic microangiopathy; aplastic anaemia;
 ischaemic injury; anorexia; diabetes; ulcerative colitis; psoriasis;
 asthma; AIDS; therapy; TRAIL receptor; TRAIL-R; AIM-I.

OS Homo sapiens.
 XX
 PN WO2003042367-A2.
 XX
 PD 22-MAY-2003.
 XX
 PF 13-NOV-2002; 2002WO-US036431.
 XX
 PR 14-NOV-2001; 2001US-0331309P.
 PR 07-MAY-2002; 2002US-0377973P.
 PR 15-AUG-2002; 2002US-0403376P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Salcedo T, Roschke V, Ruben SM, Rosen CA;
 XX
 DR WPI; 2003-449572/42.
 XX

Novel antibody against TNF-related apoptosis inducing ligand, useful for
 preventing, treating and ameliorating cancers and other
 hyperproliferative disorders, binds immunospecifically to TRAIL receptor
 PT 4 polypeptide.

XX Example 2; Page 392-393; 405pp; English.
 PS
 XX

The invention relates to antibodies that immunospecifically bind to
 tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
 receptors (TRAIL-R). Antibodies of the invention are useful for treating,
 preventing or ameliorating cancer (e.g. cancers of pancreas, uterine,
 breast, colon, lung and gastrointestinal and Kaposi's sarcoma) and other
 hyperproliferative disorders, neurodegenerative disorders (e.g.
 Parkinson's disease, Alzheimer's disease and Huntington's disease),
 autoimmune disorders (e.g. lupus, rheumatoid arthritis, multiple
 sclerosis, myasthenia gravis, Hashimoto's disease and immunodeficiency
 syndrome), inflammatory disorders (e.g. asthma, allergic disorders and
 rheumatoid arthritis), infectious diseases (e.g. acquired immune
 deficiency syndrome; AIDS, herpes viral infections and other viral
 infections), myelodysplastic syndromes (e.g. aplastic anaemia), graft-
 versus-host disease, ischaemic injury, liver injury, toxin-induced liver
 disease, septic shock, cachexia, anorexia and proliferative disorders.
 Antibodies of the invention are also useful for treating cardiovascular
 disorders, cerebrovascular disorders, thrombotic microangiopathies,
 diabetes, ocular disorders associated with neovascularisation, psoriasis,
 and ulcerative colitis and for wound healing. The invention is also used
 to prepare vaccines. The present sequence is human TRAIL protein also
 known as AIM-I

XX Sequence 281 AA;
 SQ

Query Match
 Best Local Similarity 100.0%; Score 281; DB 6; Length 281;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNKLQMDKYSGKIACFLKE 60
 DB 1 MAMMEVQGGPSLQGTCLVLIIVFTVLLQSLCAVAVYVYFTNKLQMDKYSGKIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRVLKMLRTSEETISTVQKQKQNISPLVREGPQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRVLKMLRTSEETISTVQKQKQNISPLVREGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKG 180

QY 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAKNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRQEEIKENTKNDKQWQYIYKYTSYDPDILLMKSAKNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 29
 ABU08558
 ID ABU08558 standard; protein; 281 AA.
 XX
 AC ABU08558;
 XX
 DT 05-JUN-2003 (first entry)
 DE Human TNF Related Apoptosis Inducing Ligand, TRAIL.
 XX

Human; TNF related apoptosis inducing ligand; TRAIL;
 tumour necrosis factor; apoptosis; haemostatic; immunosuppressive;
 antiinflammatory; dermatological; thrombotic microangiopathy;
 thrombotic thrombocytopenic purpura; TTP; HUS; SLE; clotting disorder;
 adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;
 systemic lupus erythematosus.

XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 PT Region 39..124

FT	/note= "N-terminal fragment specifically claimed in claim	
FT	26"	
FT	Region	124..276
FT	/note= "This region is specifically claimed in claim 20"	
FT	Region	276..281
FT	/note= "C-terminal fragment specifically claimed in claim	
FT	26"	
XX		
XX	US6521228-B1.	
PN		
XX		
XX	18-FEB-2003.	
XX		
XX	02-APR-2001; 2001US-00825563.	
XX		
XX	29-JUN-1995; 95US-00496632.	
PR	01-NOV-1995; 95US-00548368.	
PR	25-JUN-1996; 96US-00670354.	
PR	26-MAR-1998; 98US-00048641.	
PR	10-NOV-1998; 98US-00190046.	
PR	26-MAY-1999; 99US-00320424.	
XX		
XX	(IMMV) IMMUNEX CORP.	
PA		
XX		
XX	Wiley SR, Goodwin RG;	
PI		
XX		
DR	WPI; 2003-340628/32.	
DR	N-PSDB: ABX93869.	

Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIVG	281
RESULT 30			
		ABR42313	
ID		ABR42313 standard; protein; 281 AA.	
XX		AC AC	
XX		ABR42313;	
DT		11-AUG-2003 (first entry)	
XX		XX XX	
DE		Human TRAIL protein.	
XX		XX XX	
KW		Human; TRAIL; tumour necrosis factor; ligand; cytostatic;	
KW		immunomodulator; osteopathic.	
OS		XX XX	
XX		Homio sapiens.	
XX		XX XX	
BN		WO2003040307-A2.	
XX		XX XX	
PD		15-MAY-2003.	
XX		XX XX	
PF		25-JUL-2002; 2002WO-US023782.	
XX		XX XX	
PR		27-JUL-2001; 2001US-0307838P.	
XX		XX XX	
PA		(HUMA-) HUMAN GENOME SCI INC.	
XX		XX XX	
PI		Hilbert DH, Rosen CA;	
XX		XX XX	
DR		WPI; 2003-430659/40.	
XX		N-PSDB; ACC57899.	
DR		XX XX	
XX		XX XX	
PT		New heteromultimeric complex having a first polypeptide mu	
PT		tumor necrosis factor (TNF) ligand family, and a second d	
PT		of TNF ligand family, useful for treating cancer, osteop	
PT		autoimmune disease.	
XX		XX XX	
PS		Disclosure; Page 364-365; 388pp; English.	
XX		XX XX	
CC		The present sequence is the protein sequence of human TRA	
CC		The invention relates to compositions comprising heterotr	
CC		of tumour necrosis factor (TNF) ligand family members, an	
CC		the detection, prevention and treatment of disease. In on	
CC		the heterotrimeric complex comprises full-length or extra	
CC		portions of TRAIL and full-length or extracellular portio	
CC		ligand family members, preferably RANKL. The heterotrimer	
CC		the invention are useful for treating an autoimmune disea	
CC		osteoporosis, and particularly for inhibiting cancer cell	
CC		increasing B cell proliferation, or inducing apoptosis of	
CC		claimed method of inducing apoptosis of T cells comprises	
CC		heterotrimeric complex consisting of FasL and LIGHT, TNF-a	
CC		lymphotoxin-beta or TRAIL. A claimed method of inhibiting	
CC		proliferation involves administering a heterotrimeric comp	
CC		of TRAIL and CD40L or RANK. A claimed method of treating c	
CC		comprises administering an antibody against a complex comp	
CC		and TRAIL	
XX		XX XX	
		Sequence 281 AA:	
		Sequence 281 AA:	

61	DDSYWDPNDEESMNSPCWQVWQRJQLVRKWLRTSEETSTVQEKQONISPLVRERGPQ	120
Db		
QY	121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIRHEKG	180
Db	121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIRHEKG	180
QY	181 FYVYISQTYFRFOEIKENTQNDKQVQYIYKTYSTYDPPILLMKSAANSQWSKDABYGLY	240
Db	181 FYVYISQTYFRFOEIKENTQNDKQVQYIYKTYSTYDPPILLMKSAANSQWSKDABYGLY	240

Db 61 DSYWDPNDESMNSPCWQVKQLRQLVRKMLIRSEETISTVQKQKQNSPLVREGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNSCWSDAEYGLY 240
 Db 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 RESULT 31
 ABG71905
 ID ABG71905 standard; protein; 281 AA.
 AC ABG71905;
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Human TRAIL receptor-associated protein.
 XX
 KW Human; TRAIL receptor; tumour necrosis factor; TNF;
 KW light chain variable region TNF-related apoptosis-inducing ligand;
 KW antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7;
 KW TR10; apoptosis; hyperproliferative disorder; hybridoma cell line;
 KW Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease;
 KW AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; autoimmune disorder;
 KW multiple sclerosis; Behcet's disease; lupus erythematosus;
 KW inflammatory disease; rheumatoid arthritis; psoriasis; wound healing;
 KW cardiovascular disorder; angiogenesis; immune response;
 KW chemotherapeutic agent.
 XX
 OS Homo sapiens.
 XX
 PN WC200279377-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 07-NOV-2001; 2001WO-US042996.
 XX
 PR 08-NOV-2000; 2000US-0246612P.
 PR 16-NOV-2000; 2000US-0248847P.
 PR 27-NOV-2000; 2000US-0252904P.
 PR 04-JUN-2001; 2001US-0295018P.
 PR 09-OCT-2001; 2001US-0327359P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Salcedo T, Roschke V, Ruben SM, Rosen CA;
 XX
 DR WPI; 2003-040669/03.
 XX
 PT Novel antibody for treating, or preventing disease or disorder, comprises
 PT amino acid sequence having identity to other amino acid sequence of
 PT either variable heavy/light chain-complementarity determining regions.
 XX
 PS Disclosure; Page 366; 375pp; English.
 XX
 CC The invention relates to an isolated antibody comprising a first amino
 CC acid sequence having 95 % identity to a second amino acid sequence of
 CC either variable heavy chain or light chain-complementarity determining
 CC regions (VHCDRI)/VLCDR1, VHCDR2/VLCDR2 or VHCDR3/VLCDR3 appearing as
 CC ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF
 CC (tumour necrosis factor)-related apoptosis-inducing ligand receptor, also
 CC known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that
 CC produces the antibody, an antibody that binds the same epitope on a TR4
 CC polypeptide as the antibodies detailed above, detecting expression of a
 CC TR4 polypeptide (or detecting, diagnosing, prognosing or monitoring

CC cancers, and other hyperproliferative disorders) using the antibodies, a
 CC hybridoma cell line selected from the hybridoma cell lines contained in
 CC ATCC Deposit No. PTA-3149, PTA-2687, PTA-3369, PTA-2730, PTA-2729, PTA-
 CC 2728, PTA-3368, and PTA-2731 and the antibodies expressed by these
 CC hybridoma cell lines. The antibodies of the invention are useful for
 CC diagnosing or treating a disease or disorder associated with increased or
 CC decreased apoptosis, e.g. cancer (such as colon, breast, uterine,
 CC pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-
 CC host disease (GVHD), infectious disease, acquired immunodeficiency
 CC syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease), autoimmune disorders like multiple
 CC sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases
 CC such as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in
 CC promoting angiogenesis, wound healing, and in regulating immune response.
 CC Many other diseases and disorders are listed in the specification. The
 CC antibody is administered in combination with a chemotherapeutic agent
 CC selected from irinotecan, paclitaxel (TAXOL (RPM)), and gemcitabine. The
 CC antibody is useful as a diagnostic tool to monitor the expression of
 CC TRAIL receptor expression on cells, to detect, purify, and target the
 CC polypeptides, and in immunoassays for qualitatively and quantitatively
 CC measuring levels of TRAIL receptor polypeptides. The present sequence is
 CC a human TRAIL receptor associated protein. Note: The present sequence is
 CC included in the sequence listing but is not referred to anywhere else in
 CC the specification
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLKQMDKYSKSGIACFLKE 60
 Db 1 MAMVEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNKLKQMDKYSKSGIACFLKE 60
 QY 61 DSYWDPNDESMNSPCWQVKQLRQLVRKMLIRSEETISTVQKQKQNSPLVREGPQ 120
 Db 61 DSYWDPNDESMNSPCWQVKQLRQLVRKMLIRSEETISTVQKQKQNSPLVREGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIHKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNSCWSDAEYGLY 240
 Db 181 FYIYSQTYFRQEEIKENTKNDKQMVQYIYKTSYTPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 RESULT 32
 ABP60546
 ID ABP60546 standard; protein; 281 AA.
 XX
 AC ABP60546;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Human tumour necrosis factor TRAIL.
 XX
 KW APRIL; sFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antineoplastic; antirheumatic;
 KW antithrombotic; cytostatic; antianaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
 KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thymomimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; TRAIL; tumour necrosis factor.
 OS Homo sapiens.
 XX

CC disorders. They are also useful for treating myelodysplastic syndromes
 CC (e.g. aplastic anemia), ischaemic injury (such as that caused by stroke,
 CC myocardial infarction and reperfusion injury), septic shock, cachexia,
 CC anorexia and toxin-induced liver diseases (such as alcohol). They are
 CC also useful for treating cardiovascular disorders including peripheral
 CC artery diseases such as limb ischaemia, arrhythmia, congestive heart
 CC failure and cardiovascular tuberculosis, diseases or disorders associated
 CC with neovascularisation and ocular disorders, for wound healing, for
 CC promoting angiogenesis and as adjuvants to enhance immune responsiveness
 CC to specific antigen e.g. viral antigen. They are also useful in the
 CC preparation or recovery from surgery, trauma, radiation therapy and
 CC transplantation. The present sequence is human TR4 ligand, TRAIL protein
 CC used in the invention
 XX
 XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQKQNIPLVRRGPQ 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQKQNIPLVRRGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKARSNCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKARSNCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 34

AAO31151

ID AAO31151 standard; protein; 281 AA.

XX AAO31151;

XX AAO31151;

XX AAO31151;

XX 06-OCT-2003 (first entry)

XX Human TNF-related apoptosis-inducing ligand (TRAIL).

XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;

XX complementarity determining region; CDR; light chain variable domain; VL;
 XX TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
 XX DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
 XX Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
 XX glioblastoma; graft versus host disease; antibody therapy; neutropenic;
 XX AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
 XX immunosuppressive; neuroprotective; antibody therapy; antibody.

OS Homo sapiens.

XX WO2003054216-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-US040597.

XX 20-DEC-2001; 2001US-0341237P.

XX 05-APR-2002; 2002US-0369877P.

XX 04-JUN-2002; 2002US-0384828P.

XX 18-JUL-2002; 2002US-0396591P.

XX 15-AUG-2002; 2002US-0403370P.

PR 13-NOV-2002; 2002US-0425737P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;

XX WPI; 2003-569250/53.

XX New antibody or its fragment, useful for treating, preventing or

XX ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or

XX gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host

XX disease, AIDS.

XX Disclosure; Page 297-298; 301pp; English.

XX The invention relates to an isolated antibody or its fragments such as

XX VHCDR1 (heavy chain variable domain complementarity determining region),

XX VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity

XX determining region), VLCDR2 or VLCDR3. The antibody or its fragment

XX immunospecifically binds TRAIL (tumour necrosis factor; TNF-related

XX apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as

XX TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The

XX antibody or its fragment is useful for treating, preventing or

XX ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or

XX gastrointestinal cancer or Kaposi's sarcoma or cancer of the central

XX nervous system such as medulloblastoma, neuroblastoma or glioblastoma or

XX graft versus host disease, AIDS (acquired immune deficiency syndrome) or

XX a neurodegenerative disorder. The invention is useful in antibody

XX therapy. The present sequence is human TRAIL

XX Sequence 281 AA;

XX Query Match 100.0%; Score 281; DB 6; Length 281;

XX Best Local Similarity 100.0%; Pred. No. 1.8e-266;

XX Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60

DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKGIACFLKE 60

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQKQNIPLVRRGPQ 120

DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQKQNIPLVRRGPQ 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180

DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKARSNCWSKDAEYGLY 240

DB 181 FYIYSQTYFRFOEIKENTKNDKQVYIYKTSYPPDILLMKARSNCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 35

ABO25125

ID ABO25125 standard; protein; 281 AA.

XX ABO25125;

XX ABO25125;

XX 05-SEP-2003 (first entry)

XX Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.

XX Human; DNA methylation; cancer; colon cancer.

XX Homo sapiens.

XX US2003013099-A1.

XX

PD 16-JAN-2003.
 XX
 PF 07-MAR-2002; 2002US-00093766.
 XX
 PR 19-MAR-2001; 2001US-0277380P.
 XX
 PA (LASE/) LASEK A X W.
 PA (JONES/) JONES D A.
 PA (KARP/) KARP A R.
 XX
 PI Lasek AKW, Jones DA, Karpf AR;
 XX
 DR WPI; 2003-503249/47.
 DR N-PSDB; ACD42246.
 XX
 PT New combination comprising cDNAs that are expressed in a disorder or
 PT process associated with DNA methylation, useful for diagnosing, staging,
 PT treating or monitoring treatment of cancer, e.g. colon cancer.
 PS Disclosure; Page 56-57; 66pp; English.
 XX
 CC The invention relates to a combination comprising cDNAs which are
 CC expressed in a disorder or process associated with DNA methylation. The
 CC combination and cDNAs are useful for diagnosing, staging, treating or
 CC monitoring treatment of cancer, e.g. colon cancer, and for detecting
 CC changes in expression of genes encoding proteins that are associated with
 CC DNA methylation. The protein is useful for screening molecules or
 CC compounds to identify at least one ligand that binds to the protein and
 CC for producing an antibody. The present sequence represents the amino acid
 CC sequence of a protein expressed in a disorder or process associated with
 CC DNA methylation
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 6; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 DB 61 DDSYWDPNDEESMNSPCWQVKQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 36
 ID ADB61471
 XX ADB61471 standard; protein; 281 AA.
 AC ADB61471;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Native human Apo-2 ligand protein.
 XX
 KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;

KW native; human.
 XX Homo sapiens.
 OS WO2003029420-A2.
 PN 10-APR-2003.
 XX
 PD 01-OCT-2002; 2002WO-US031210.
 XX
 PR 02-OCT-2001; 2001US-0326622P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Kelley RF, Lindstrom SH;
 XX
 DR WPI; 2003-541400/51.
 DR N-PSDB; ADB61470.
 XX
 PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 PS Claim 1; Fig 1; 92pp; English.
 XX
 CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the native human Apo-2 ligand protein of
 CC the invention.
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVYFTNELKQMDKYSKGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 DB 61 DDSYWDPNDEESMNSPCWQVKQLRVLVRKMLTSEETISTVQEKQNTSPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIREKG 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNCSWCKDAEYGLY 240

Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
RESULT 37
ADC35202
ID ADC35202 standard; protein; 281 AA.
AC ADC35202;
XX
XX 18-DEC-2003 (first entry)
DT
DE Human TNF ligand family member #10.
XX
XX human; tumour necrosis factor; TNF ligand; endokine alpha;
KW excessive bone resorption disorder; osteoporosis; Paget's disease;
KW arterial calcification.
XX
XX Homo sapiens.
OS
XX US2003100074-A1.
PN
XX 29-MAY-2003.
PD
XX 15-AUG-2002; 2002US-00218547.
XX
XX 16-AUG-2001; 2001US-0312542P.
PR 30-OCT-2001; 2001US-0330761P.
XX
XX (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (NARD/) NARDELLI B.
XX
PI Yu G, Ni J, Rosen CA, Nardelli B;
XX
XX WPI; 2003-696072/66.
DR N-PSDB; ADC35201.
XX
XX New Endokine alpha gene useful for preparing a composition for treating a
PT disease associated with excessive or insufficient bone resorption e.g.,
PT osteoporosis, Paget's disease or arterial calcification.
XX
XX Disclosure; SEQ ID NO 20; 145pp; English.
PS
XX The invention relates to an isolated nucleic acid molecule encoding a
CC tumour necrosis factor family ligand. A composition comprising the
CC isolated antibody or its fragment is used for treating an individual in
CC need of decreased level of endokine alpha activity. The endokine alpha
CC polypeptide present in a heterotrimeric complex is used for treating an
CC individual having a disorder associated with excessive bone resorption,
CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
CC individual having a disorder associated with insufficient bone resorption
CC comprises administering an endokine alpha antagonist, which is the
CC antibody that binds specifically to endokine alpha polypeptide. The
CC present sequence represents the amino acid sequence of a tumour necrosis
CC factor family ligand.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 281; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-266;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTYVTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTYVTNELKQMDKYSGIACFLKE 60
QY 61 DSYWDPNDESMNSPCWQVKQLRQVLMILRTSETISTVQEKQONISPLVERGPQ 120

Db 61 DSYWDPNDESMNSPCWQVKQLRQVLMILRTSETISTVQEKQONISPLVERGPQ 120
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
Db 131 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDILLMKARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
RESULT 38
ADD14080
ID ADD14080 standard; protein; 281 AA.
XX
AC ADD14080;
XX
XX 01-JAN-2004 (first entry)
DT
DE Human src biomarker polypeptide SEQ ID NO:269.
XX
XX predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human.
XX
XX Homo sapiens.
OS
XX WO2003062395-A2.
PN
XX 31-JUL-2003.
PD
XX 17-JAN-2003; 2003WO-US0011981.
XX
XX 18-JAN-2002; 2002US-0350061P.
PR
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Huang F, Fairchild CR, Lee FY, Shaw P;
PI WPI; 2003-636735/60.
XX
XX N-PSDB; ADD14676.
DR
XX New polynucleotides and polypeptides for predicting the activity of
PT compounds that interact with protein tyrosine kinases and/or protein
PT tyrosine kinase pathways.
XX
XX Claim 10; SEQ ID NO 269; 139pp; English.
PS
XX The present invention describes a predictor set comprising a plurality of
CC polynucleotides or polypeptides whose expression pattern is predictive of
CC the response of cells to treatment with a compound that modulates protein
CC tyrosine kinase activity or members of the protein tyrosine kinase
CC pathway. Also described: (1) predicting whether a compound is capable of
CC modulating the activity of cells, comprising obtaining a sample of cells,
CC determining whether the cells express a plurality of markers, and
CC correlating the expression of the markers to the compound's ability to
CC modulate the activity of the cells; (2) a plurality of cell lines for
CC identifying polynucleotides and polypeptides whose expression levels
CC correlate with compound sensitivity or resistance of cells associated
CC with a disease state; and (3) identifying polynucleotides and
CC polypeptides that predict compound sensitivity or resistance of cells
CC associated with a disease state, comprising subjecting the plurality of
CC cell lines to one or more compounds, analysing the expression pattern of
CC a microarray of polynucleotides or polypeptides, and selecting
CC polynucleotides or polypeptides that predict the sensitivity or
CC resistance of cells associated with a disease state by using the
CC expression pattern of the microarray. The polynucleotides and
CC polypeptides have cytostatic activities, and can be used in gene therapy.
XX The polynucleotides and polypeptides are useful in predicting the

CC activity of compounds that interact with protein tyrosine kinases and/or
 CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC genetic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTISPLVRERG 120
 DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTISPLVRERG 120

QY 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180
 DB 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOBEIKENTKDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOBEIKENTKDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 39

ID ADD19010
 XX ADD19010 standard; protein; 281 AA.

AC ADD19010;

DT 15-JAN-2004 (first entry)

XX Human disease related protein SeqID499.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
 XX antiarteriosclerotic; vulnary; gene therapy;
 XX hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 XX inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 XX glucose transportation; catecholamine synthesis; iron transport;
 XX nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 XX retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 XX inflammatory condition; wound healing.

XX Homo sapiens.

XX W02003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002W0-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX N-PSDB; ADD19011.

XX New substantially purified polypeptide, useful for diagnosing or treating
 XX a hypoxia-regulated condition, such as cancer, ischemia, reperfusion

PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.

XX Claim 25; SEQ ID NO 499; 424pp; English.

XX This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory, the
 CC ophthalmological, antiarteriosclerotic or vulnary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.

XX Sequence 281 AA;

Query Match 100.0%; Score 281; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

DB 1 MAMMEVGGPSLGTCLVIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTISPLVRERG 120

DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQNTISPLVRERG 120

QY 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180

DB 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHG 180

QY 181 FYIYSQTYFRFOBEIKENTKDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240

DB 181 FYIYSQTYFRFOBEIKENTKDKQVQYIYKYTSYDPDILLMKSARNCSKDAEYGLY 240

QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 40

ADDE76953

ID ADE76953 standard; protein; 281 AA.

XX ADE76953;

DT 29-JAN-2004 (first entry)

XX Human protein expressed in a liver disorder #32.

XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
 KW tumour; liver; inflammatory disorder; immune response disorder;
 KW high-throughput screening; differential gene expression; gene therapy.

XX Homo sapiens.

XX US2003108871-A1.

XX 12-JUN-2003.

XX 30-JUL-2001; 2001US-00919039.

XX 28-JUL-2000; 2000US-0222113P.

XX (KASE/) KASER M R.

PI Kaser MR;
 DR WPI; 2004-031227/03.
 DR N-PSDB; ADE76952.
 XX
 XX Composition comprising several cDNAs that are differentially expressed in
 PT treated human C3A liver cell cultures, useful for treating liver
 PT disorders.
 XX
 XX Claim 1; SEQ ID NO 118; 41pp; English.
 XX
 XX The invention relates to a composition comprising several cDNAs that are
 CC differentially expressed in a liver disorder. The composition is useful
 CC for treating liver disorder such as hyperlipidaemia, hypertension, type
 CC II diabetes, tumours of the liver and disorders of the inflammatory and
 CC immune response. The composition is useful for a high-throughput method
 CC of screening several molecules or compounds to identify a ligand which
 CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
 CC high-throughput method for using a protein to screen several molecules or
 CC compounds to identify at least one ligand which specifically binds the
 CC protein which involves combining the protein encoded by the cDNA with
 CC several of molecules or compounds under conditions to allow specific
 CC binding, and detecting specific binding between the protein and a
 CC molecule or compound, therefore identifying a ligand which specifically
 CC binds the protein. The composition is useful for detecting and
 CC quantifying differential gene expression, can be used in gene therapy, to
 CC formulate prognosis and to design a treatment regimen and to monitor the
 CC efficacy of treatment. The present sequence represents the amino acid
 CC sequence of a protein encoded by a cDNA differentially expressed in a
 CC liver disorder.
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 281; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-266;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1. MAMVEVGGPSLGQTCVLIVFTVLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60
 Db 1 MAMVEVGGPSLGQTCVLIVFTVLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKE 60
 QY 61 DSDYNDPNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGPG 120
 Db 61 DSDYNDPNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGPG 120
 QY 121 RVAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
 Db 121 RVAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKG 180
 QY 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKARSNCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKARSNCWSKDAEYGLY 240
 QY 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 41
 AAW76332
 ID AAW76332 standard; protein; 279 AA.
 XX
 AC AAW76332;
 XX
 XX 11-JAN-1999 (first entry)
 DE Human TL2 (TRAIL), ligand for TR5.
 KW TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;
 KW arthritis; septicaemia; transplant rejection; autoimmune disease;
 KW inflammatory bowel disease; graft versus host disease; infection; stroke;
 KW ischaemia; acute respiratory disease syndrome; psoriasis; restenosis;
 KW brain injury; AIDS; bone disease; cancer; atherosclerosis;

KW Alzheimer's disease; human; therapy; diagnosis; ligand.
 XX Homo sapiens.
 XX EP867509-A2.
 XX 30-SEP-1998.
 XX 04-FEB-1998; 98EP-00300827.
 XX 05-FEB-1997; 97US-00795910.
 XX 28-JUL-1997; 97US-00901469.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Young PR, Tan KB, Truneh A, Lyn SDP;
 XX WPI; 1998-497862/43.
 XX New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent
 PT and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases,
 PT infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,
 PT AIDS and bone diseases.
 XX Disclosure; Page 17-18; 22pp; English.
 XX This is the amino acid sequence of human TL2 (also known as TRAIL), which
 CC has newly been discovered to be a ligand of human tumour necrosis related
 CC receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and
 CC TL2 can be used in screening processes for compounds which bind the
 CC receptor, or its ligand, and which activate (agonists) or inhibit
 CC (antagonists) the receptor or TL2. Treatment of a subject with the need
 CC to inhibit TR5 polypeptide activity comprises administering an antagonist
 CC to the polypeptide, administering a nucleic acid that inhibits the
 CC expression of the nucleotide sequence encoding the polypeptide and/or
 CC administering a polypeptide that competes with the polypeptide for its
 CC ligand, substrate or receptor. The active agents can be used for the
 CC treatment of chronic and acute inflammation, arthritis, septicaemia,
 CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),
 CC transplant rejection, graft vs host disease, infection, stroke,
 CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,
 CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),
 CC atherosclerosis and Alzheimer's disease
 XX SQ Sequence 279 AA;
 Query Match 99.3%; Score 279; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.6e-264;
 Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKEDD 62
 Db 1 MMEVQGGPSLGQTCVLIVFTVLQSLCAVAVTVVYFTNKLQMDKYSGIACFLKEDD 60
 QY 63 SYNDPNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGPG 122
 Db 61 SYNDPNDDESMNSPCQVQKWQLRQLVRKMLRTSEETISTVQEKQNIPLVRGPG 120
 QY 123 AAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKGFY 182
 Db 121 AAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHEKGFY 180
 QY 183 YIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKARSNCWSKDAEYGLY 242
 Db 181 YIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYPPDILLMKARSNCWSKDAEYGLY 240
 QY 243 YQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 YQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279
 RESULT 42
 AAW95032

AAW95032 standard; protein; 279 AA.
AAW95032;
13-MAY-1999 (first entry)
Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
inflammation; septicemia; autoimmune disease; transplant rejection;
graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
acute respiratory disease syndrome; restenosis, bone disease; cancer;
atherosclerosis; Alzheimer's disease.
Unidentified.
EP897114-A2.
17-FEB-1999.
04-JUN-1998; 98EP-00304424.
13-AUG-1997; 97US-0055513P.
26-AUG-1997; 97US-0056980P.
29-AUG-1997; 97US-0057550P.
(SMIK) SMITHKLINE BEECHAM CORP.
Brigham-Burke MR, Young PR;
WPI; 1999-134308/12.
Identifying agonists and antagonists to tumour necrosis factor receptor
(TNF-R) related polypeptides (LRI, LR2, LT2 and LT4) - useful for
treating stroke, Alzheimer's disease and AIDS.
Disclosure; Page 14-15; 18pp; English.
The invention relates to identifying agonists or antagonists to tumour
necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
assessing the ability of the candidate compound to compete with TR1 or
TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
for treating diseases caused by imbalance of TR or TR polypeptide levels,
which cause: chronic and acute inflammation, arthritis, septicemia,
autoimmune diseases, transplant rejection, graft vs. host disease,
infection, stroke, ischemia, acute respiratory disease syndrome,
restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
Alzheimer's disease. The present sequence represents a TNF-R related
polypeptide TL2
SQ Sequence 279 AA;
Query Match 99.3%; Score 279; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYKSGIACFLKEDD 62
DB 1 MMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYKSGIACFLKEDD 60
QY 63 SYNDPNDDESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRGRQV 122
DB 61 SYNDPNDDESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRGRQV 120
QY 123 AAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHKGFY 182
DB 121 AAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHKGFY 180
QY 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSGARNCSWKDAEYGLYSI 242
AAW95032 standard; protein; 279 AA.
AAW95032;
13-MAY-1999 (first entry)
Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
inflammation; septicemia; autoimmune disease; transplant rejection;
graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
acute respiratory disease syndrome; restenosis, bone disease; cancer;
atherosclerosis; Alzheimer's disease.
Unidentified.
EP897114-A2.
17-FEB-1999.
04-JUN-1998; 98EP-00304424.
13-AUG-1997; 97US-0055513P.
26-AUG-1997; 97US-0056980P.
29-AUG-1997; 97US-0057550P.
(SMIK) SMITHKLINE BEECHAM CORP.
Brigham-Burke MR, Young PR;
WPI; 1999-134308/12.
Identifying agonists and antagonists to tumour necrosis factor receptor
(TNF-R) related polypeptides (LRI, LR2, LT2 and LT4) - useful for
treating stroke, Alzheimer's disease and AIDS.
Disclosure; Page 14-15; 18pp; English.
The invention relates to identifying agonists or antagonists to tumour
necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
assessing the ability of the candidate compound to compete with TR1 or
TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
for treating diseases caused by imbalance of TR or TR polypeptide levels,
which cause: chronic and acute inflammation, arthritis, septicemia,
autoimmune diseases, transplant rejection, graft vs. host disease,
infection, stroke, ischemia, acute respiratory disease syndrome,
restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
Alzheimer's disease. The present sequence represents a TNF-R related
polypeptide TL2
SQ Sequence 279 AA;
Query Match 99.3%; Score 279; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 MMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYKSGIACFLKEDD 62
DB 1 MMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYKSGIACFLKEDD 60
QY 63 SYNDPNDDESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRGRQV 122
DB 61 SYNDPNDDESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRGRQV 120
QY 123 AAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHKGFY 182
DB 121 AAHTGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLNGELVIEHKGFY 180
QY 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSGARNCSWKDAEYGLYSI 242

Db 181 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYPPDPILLMKSGARNCSWKDAEYGLYSI 240
QY 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 279
RESULT 43
AAW27018
ID AAY27018 standard; protein; 281 AA.
XX AC AAY27018;
XX DT 24-SEP-1999 (first entry)
XX DE Human Apo-2 ligand (Apo-2L) variant D269A.
XX KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
XX KW lupus; immune-mediated glomerular nephritis; human; variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 269 /label= D269A
XX FT /note= "wild-type Asp is replaced with Ala"
XX PN WO9936535-A1.
XX PD 22-JUL-1999.
XX PF 15-JAN-1999; 99WO-US001039.
XX PR 15-JAN-1998; 98US-00007886.
XX PR 15-APR-1998; 98US-00060533.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
in mammalian cancer cells.
XX Claim 11; Page; 86pp; English.
XX The invention relates to a novel human cytokine, designated Apo-2 ligand
(Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
cells. This is useful for the treatment of cancer. Apo-2L can be used to
induce apoptosis for pathological conditions characterized by decreased
levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
coding sequence can also be used in quantitative and screening diagnostic
techniques. Anti-Apo-2L antibodies can be used for treating diseases
associated with increased apoptosis. Sequences AAY27016-19 represent
specific examples of Apo-2L variants. Note: This sequence is not provided
in the specification. It has been created by modifying the wild-type Apo-
2L sequence provided in Fig 1A
SQ Sequence 281 AA;
Query Match 95.4%; Score 268; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 9.6e-254;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYDPNDDESNNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRGRQV 120

Db 61 DSYWDPNDEESNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSGARNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSGARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDM 268
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDM 268

RESULT 44

ADB61495

ID ADB61495 standard; protein; 281 AA.

XX AC ADB61495;

XX DT 04-DEC-2003 (first entry)

XX DE Human Apo-2 ligand protein mutant H264C.

XX KW Apo-2 ligand; DR5-Apo2L complex; receptor contact region;

XX KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;

XX KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;

XX KW lung; breast; immune-related disease; arthritis; multiple sclerosis;

XX KW human; mutant; mutein.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key

XX FH Location/Qualifiers

XX FT Misc-difference 264

XX FT /note= "Native residue of His is substituted by Cys"

XX FN WO2003029420-A2.

XX XX 10-APR-2003.

XX PF 01-OCT-2002; 2002WO-US031210.

XX PR 02-OCT-2001; 2001US-0326622P.

XX PA (GETH) GENENTECH INC.

XX PI Kelley RF, Lindstrom SH;

XX DR WPI; 2003-541400/51.

XX XX

XX PT Novel isolated Apo-2 ligand variant polypeptide useful for treating

XX PT cancer or an immune-related disease such as multiple sclerosis, comprises

XX PT amino acid substitutions in the native sequence of the Apo-2 ligand.

XX PS Claim 1; Page; 92pp; English.

XX XX

XX CC The invention relates to a novel isolated Apo-2 ligand variant

XX CC polypeptide having a sequence that differs from the native sequence

XX CC having 281 amino acids given in specification. The Apo-2 ligand variant

XX CC polypeptide is selected from a polypeptide having substitutions at

XX CC residue positions identified from x-ray crystal structure of the

XX CC DR5-Apo2L complex. The polypeptide having the substitutions made at

XX CC residue position(s) selected from 20 positions such as S96C, S101C,

XX CC S111C, V114C, R115C, N134C, N140C, E144C, N152C, S153C, R170C,

XX CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the

XX CC residue position is, outside of the receptor contact region of the

XX CC DR5-Apo2L complex, and displays high solvent accessibility in the crystal

XX CC structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide

XX CC and further compositions have the following activities: cytostatic,

XX CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,

CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant H264C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX SQ Sequence 281 AA;

Query Match

Best Local Similarity 93.6%; Score 263; DB 7; Length 281;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGGTGVILVIFVTLVLOSCLVAVTVVYFTNELKQMDKYSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGGTGVILVIFVTLVLOSCLVAVTVVYFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
 Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVTHEKG 180
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHGFSLNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSGARNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRQEEIKENTKNDKQWQVIYKYTSYPPDPILLMKSGARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNE 263
 Db 241 SIYQGGIFELKENDRIFVSVTNE 263

RESULT 45

ADB61494

ID ADB61494 standard; protein; 281 AA.

XX AC ADB61494;

XX DT 04-DEC-2003 (first entry)

XX DE Human Apo-2 ligand protein mutant E263C.

XX KW Apo-2 ligand; DR5-Apo2L complex; receptor contact region;

XX KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;

XX KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;

XX KW lung; breast; immune-related disease; arthritis; multiple sclerosis;

XX KW human; mutant; mutein.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key

XX FH Location/Qualifiers

XX FT Misc-difference 263

XX FT /note= "Native residue of Glu is substituted by Cys"

XX FN WO2003029420-A2.

XX XX 10-APR-2003.

XX PF 01-OCT-2002; 2002WO-US031210.

XX PR 02-OCT-2001; 2001US-0326622P.

XX PA (GETH) GENENTECH INC.
XX PI Kelley RF, Lindstrom SH;
XX DR WPI; 2003-541400/51.
XX
PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
PS Claim 1; Page; 92pp; English.
XX
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5.Apo2L complex. The polypeptide having the substitutions made at
CC residue position(s) selected from 20 positions such as S96C, S101C,
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, S153C, R170C,
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant E263C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in claim 1
CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 93.2%; Score 262; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 7.2e-248;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVIFVTFVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVIFVTFVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSVWDNDESMNSPCWQVKWQLRQLVRKMLTSETSTVQEKQONTSPLVREGRQ 120
Db 61 DDSVWDNDESMNSPCWQVKWQLRQLVRKMLTSETSTVQEKQONTSPLVREGRQ 120
QY 121 RVAAHITGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
Db 121 RVAAHITGRSNTLSSPNKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
QY 181 FYYISQTYFRFBEIKENTKNDKQVQYIKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
Db 181 FYYISQTYFRFBEIKENTKNDKQVQYIKYTSYDPDILLMKASRNSCWSKDAEYGLY 240
QY 241 SIYGGIFELKENDRIFSVTN 262
Db 241 SIYGGIFELKENDRIFSVTN 262

RESULT 46
ADB61493
ID ADB61493 standard; protein; 281 AA.

XX AC ADB61493;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human Apo-2 ligand protein mutant R255C.
XX
KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutein.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 255 /note= "Native residue of Arg is substituted by Cys"
FT WO2003029420-A2.
XX
PD 10-APR-2003.
XX
PF 01-OCT-2002; 2002WO-US031210.
XX
PR 02-OCT-2001; 2001US-0326622P.
XX
PA (GETH) GENENTECH INC.
PI Kelley RF, Lindstrom SH;
XX
DR WPI; 2003-541400/51.
XX
PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
PS Claim 1; Page; 92pp; English.
CC
CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5.Apo2L complex. The polypeptide having the substitutions made at
CC residue position(s) selected from 20 positions such as S96C, S101C,
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, S153C, R170C,
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant R255C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in claim 1
CC and from the sequence in Fig 1 of the specification.
XX
SQ Sequence 281 AA;

Query Match 90.4%; Score 254; DB 7; Length 281;

Best Local Similarity 100.0%; Pred. No. 4.8e-240;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTYSPDPILLMKSAKNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTYSPDPILLMKSAKNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKEND 254
DB 241 SIYQGGIFELKEND 254

RESULT 47
ADB61492
ID ADB61492 standard; protein; 281 AA.
XX AC ADB61492;
XX DT 04-DEC-2003 (first entry)
XX DE Human Apo-2 ligand protein mutant E249C.
XX KW Apo-2 ligand; DR5 Apo2L complex; receptor contact region;
KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutein.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 249 /note= "Native residue of Glu is substituted by Cys"
XX FT
XX PN WO2003029420-A2.
XX PD 10-APR-2003.
XX PF 01-OCT-2002; 2002WO-US031210.
XX PR 02-OCT-2001; 2001US-0326622P.
XX PA (GETH) GENENTECH INC.
XX PI Kelley RF, Lindstrom SH;
XX DR WPI; 2003-541400/51.
XX PT Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX PS Claim 1; Page; 92pp; English.
XX CC The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5 Apo2L complex. The polypeptide having the substitutions made at

CC residue position(s) selected from 20 positions such as 896C, S101C,
CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5 Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5 Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant E249C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in Claim 1
CC and from the sequence in Fig 1 of the specification.
XX SQ Sequence 281 AA;

Query Match 88.3%; Score 248; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.6e-234;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
QY 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYDNDPDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTYSPDPILLMKSAKNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOBEIKENTKNDKQMVQYIYKTYSPDPILLMKSAKNSCWSDAEYGLY 240
QY 241 SIYQGGIF 248
DB 241 SIYQGGIF 248

RESULT 48
AAV01516
ID AAV01516 standard; peptide; 281 AA.
XX AC AAV01516;
XX DT 27-MAY-1999 (first entry)
XX DR Protein associated with neurodegenerative and autoimmune diseases.
XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 245 /note= "Gly or Cys"
XX FT
XX PN FR2766713-A1.
XX XX

PD 05-FEB-1999.
 XX
 PF 04-AUG-1997; 97FR-000101176.
 XX
 PR 04-AUG-1997; 97FR-000101176.
 XX
 PA (INMR) BIO MERIEUX.
 XX
 PI Rieger F, Belliveau JF, Perron H;
 XX
 XX WPI; 1999-156177/14.
 XX
 DR Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.
 XX
 XX Claim 1; Page 13; 21pp; French.
 XX
 XX The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative disease, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex
 XX
 XX Sequence 281 AA;
 SQ
 Query Match 86.8%; Score 244; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3e-230;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSGIACFLKE 60
 Db 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETSTVQEKQNIISPLVRERGPO 120
 Db 61 DDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEETSTVQEKQNIISPLVRERGPO 120
 QY 121 RVAAHITGTRSNLTSSPNKSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 Db 121 RVAAHITGTRSNLTSSPNKSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNSCWSKDAEYGLY 240
 Db 181 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQ 244
 Db 241 SIYQ 244
 RESULT 49
 ID AA72935
 AC AA72935 standard; protein; 266 AA.
 AC AA72935;
 XX
 DT 11-SEP-2003 (revised)
 DT 13-JUN-2001 (first entry)
 XX
 DE OmpA signal peptide-human TRAIL fusion protein.
 XX
 XX Human; attenuated tumour-targeted bacteria; effector molecule;
 KW tumour necrosis factor; TNF; anti-angiogenic factor;
 KW cytotoxic polypeptide; tumour inhibitory enzyme; therapy; carcinoma;
 KW melanoma; lymphoma; sarcoma; metastasis; cytostatic; fusion protein;

TNF-alpha-related apoptosis-inducing ligand; TRAIL.
 KW Homo sapiens.
 XX Escherichia coli.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= OmpA_signal_peptide
 FT 23..266
 FT /note= "Mature human TNF-alpha-related apoptosis-inducing
 FT ligand"
 XX
 XX W0200125397-A2.
 PN
 XX 12-APR-2001.
 PD
 XX 24-AUG-2000; 2000WO-US023242.
 PF
 XX 04-OCT-1999; 99US-0157500P.
 PR 04-OCT-1999; 99US-0157581P.
 PR 04-OCT-1999; 99US-0157637P.
 XX
 PA (VION-) VION PHARM INC.
 XX
 XX Bermudes DG, King IC, Clairmont CA, Lin SL, Belcourt M;
 PI
 XX WPI; 2001-245063/25.
 XX N-PSDB; AAD03112.
 DR
 XX Attenuated tumor-targeted bacteria comprising nucleic acids encoding
 PT primary and secondary effector molecules, useful for the treatment of
 PT e.g. carcinomas, melanomas, lymphomas and sarcomas.
 XX
 XX Example 7; Fig 6; 185pp; English.
 PS
 XX The present invention relates to the preparation and use of attenuated
 CC tumour-targeted bacteria, such as, e.g., Salmonella, as a vector for the
 CC delivery of one or more primary effector molecules and secondary effector
 CC molecules to the site of a solid tumour. The primary effector molecules
 CC of the invention include members of the tumour necrosis factor (TNF),
 CC anti-angiogenic factors, cytotoxic polypeptides and tumour inhibitory
 CC enzymes. They induce a local immune response at the site of the tumour
 CC that results in the inhibition of growth of a tumour or tumour cells. The
 CC primary effector molecules are used for the treatment of solid tumours
 CC such as carcinomas, melanomas, lymphomas, sarcomas or metastases derived
 CC from these tumours. The present sequence is OmpA signal peptide-mature
 CC human TNF-alpha-related apoptosis-inducing ligand (TRAIL) fusion protein.
 CC The fusion of OmpA signal peptide to the amino terminus of TRAIL effector
 CC molecule enhances the periplasmic localisation and subsequent processing
 CC of the effector molecule. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 266 AA;

Query Match 86.1%; Score 242; DB 4; Length 266;
 Best Local Similarity 100.0%; Pred. No. 2.6e-228;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 NELKQMDKYSGIACFLKEDDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEET 99
 Db 25 NELKQMDKYSGIACFLKEDDSYWDNDDESNMSPCWQVKWQLRQLVRKMLRTSEET 84
 QY 100 ISTVQEKQNIISPLVRERGPOVAAHITGTRSNLTSSPNKSKNEKALGRKINSWESSRS 159
 Db 85 ISTVQEKQNIISPLVRERGPOVAAHITGTRSNLTSSPNKSKNEKALGRKINSWESSRS 144
 QY 160 GHSFSLNHLRNGELVTHEKGFYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPP 219
 Db 145 GHSFSLNHLRNGELVTHEKGFYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPP 204
 QY 220 ILLMKSARNSCWSKDAEYGLIYQGGIFELKENDRIFVSVTNEHLIDMDHASFPGAPL 279

Db 205 ILLMKARSNCWSKDAEYGLISYIOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGFL 264

QY 280 VG 281
||
Db 265 VG 266

RESULT 50
ADB61491
ID ADB61491 standard; protein; 281 AA.
XX ADB61491;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human Apo-2 ligand protein mutant D234C.
XX
KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutin.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 234
FT /note= "Native residue of Asp is substituted by Cys"
XX
XX
PN WO2003029420-A2.
XX
XX 10-APR-2003.
XX
XX 01-OCT-2002; 2002WO-US031210.
XX
XX 02-OCT-2001; 2001US-0326622P.
XX
XX (GETH) GENENTECH INC.
XX
XX Kelley RF, Lindstrom SH;
XX
XX WPI; 2003-541400/51.
XX
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
XX cancer or an immune-related disease such as multiple sclerosis, comprises
XX amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
XX Claim 1; Page; 92pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
XX polypeptide having a sequence that differs from the native sequence
XX having 281 amino acids given in specification. The Apo-2 ligand variant
XX polypeptide is selected from a polypeptide having substitutions at
XX residue positions identified from x-ray crystal structure of the
XX DR5.Apo2L complex. The polypeptide having the substitutions made at
XX residue position(s) selected from 20 positions such as S96C, S101C,
XX S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
XX R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
XX residue position is, outside of the receptor contact region of the
XX DR5.Apo2L complex, and displays high solvent accessibility in the crystal
XX structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
XX and further compositions have the following activities: cytostatic,
XX antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
XX an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
XX inducing apoptosis in mammalian cells, by exposing mammalian cells
XX expressing a receptor selected from DR4 receptor and DR5 receptor to a
XX therapeutically effective amount of the Apo-2 ligand variant polypeptide,
XX Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
XX colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
XX the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
XX treating cancer (such as lung, breast, colon or colorectal cancer) or an
XX immune-related disease (such as arthritis or multiple sclerosis) in a

CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant D234C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in claim 1
CC and from the sequence in Fig 1 of the specification.
XX
SQ Sequence 281 AA;

Query Match 82.9%; Score 233; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.7e-219;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGSPSLGQTCVLIVIFVTLQSLCVAIVYVYFTNELKQMDKYKSGIACFLKE 60
||
Db 1 MAMMEVGGSPSLGQTCVLIVIFVTLQSLCVAIVYVYFTNELKQMDKYKSGIACFLKE 60
||
QY 61 DDSYWDNDDESMNSPCQVQKWLQRLVRKWLTLTSETISTVQEKQNTSPLVRERGPO 120
||
Db 61 DDSYWDNDDESMNSPCQVQKWLQRLVRKWLTLTSETISTVQEKQNTSPLVRERGPO 120
||
QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHG 180
||
Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNHLRNGELVIEHG 180
||
QY 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPPILLMKARSNCWSK 233
||
Db 181 FYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDPPILLMKARSNCWSK 233
||
RESULT 51
RAY27017
ID AAY27017 standard; protein; 281 AA.
XX
XX AAY27017;
XX
XX 24-SEP-1999 (first entry)
XX
XX Human Apo-2 ligand (Apo-2L) variant D218A.
XX
XX Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
XX lupus; immune-mediated glomerular nephritis; human; variant.
XX
XX Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 218
FT /label= D218A
FT /note= "wild-type Asp is replaced with Ala"
XX
XX WO9936535-A1.
XX
XX 22-JUL-1999.
XX
XX 15-JAN-1999; 99WO-US001039.
XX
XX 15-JAN-1998; 98US-00007886.
XX
XX 15-APR-1998; 98US-00060533.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
XX
XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX in mammalian cancer cells.
XX
XX Claim 10; Page; 86pp; English.
XX
XX The invention relates to a novel human cytokine, designated Apo-2 ligand
XX (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant

methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-2L can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autoimmune disorders like lupus and immune-mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-2L antibodies can be used for treating diseases associated with increased apoptosis. Sequences AAY27016-19 represent specific examples of Apo-2L variants. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type Apo-2L sequence provided in Fig 1A

Sequence 281 AA;

Query Match 77.2%; Score 217; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 8e-204;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
QY 181 FYYISQTYFRFOEIKENTKNDKQMYIYKYTSYP 217
DB 181 FYYISQTYFRFOEIKENTKNDKQMYIYKYTSYP 217

RESULT 52

AAY27019

ID AAY27019 standard; protein; 281 AA.

AC AAY27019;

24-SEP-1999 (first entry)

Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.

Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human; variant.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

Misc-difference 203 /label= D203A

/note= "wild-type Asp is replaced with Ala"

Misc-difference 218 /label= D218A

/note= "wild-type Asp is replaced with Ala"

Misc-difference 269 /label= D269A

/note= "wild-type Asp is replaced with Ala"

WO9936535-A1.

22-JUL-1999.

15-JAN-1999; 99WO-US001039.

15-JAN-1998; 98US-00007886.

15-APR-1998; 98US-00060533.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
XX WPI; 1999-444397/37.
DR A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
XX in mammalian cancer cells.
XX Claim 12; Page; 86pp; English.
PS The invention relates to a novel human cytokine, designated Apo-2 ligand
CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
CC induce apoptosis for pathological conditions characterized by decreased
CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
CC coding sequence can also be used in quantitative and screening diagnostic
CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
CC associated with increased apoptosis. Sequences AAY27016-19 represent
CC specific examples of Apo-2L variants. Note: This sequence is not provided
CC in the specification. It has been created by modifying the wild-type Apo-
XX 2L sequence provided in Fig 1A
XX Sequence 281 AA;

Query Match 71.9%; Score 202; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e-189;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLQGTCLVIFVTLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVKMLRTSEETISTVQEKQONISPLVRERGPO 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
QY 181 FYYISQTYFRFOEIKENTKN 202
DB 181 FYYISQTYFRFOEIKENTKN 202

RESULT 53

AAY27016

ID AAY27016 standard; protein; 281 AA.

AC AAY27016;

24-SEP-1999 (first entry)

Human Apo-2 ligand (Apo-2L) variant D203A.

Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder; lupus; immune-mediated glomerular nephritis; human; variant.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

Misc-difference 203 /label= D203A

/note= "wild-type Asp is replaced with Ala"

WO9936535-A1.

22-JUL-1999.

15-JAN-1999; 99WO-US001039.

PR 15-JAN-1998; 98US-00007886.
 PR 15-APR-1998; 98US-00060533.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;
 PI WPI; 1999-444397/37.
 DR A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 XX in mammalian cancer cells.
 XX Claim 9; Page; 86pp; English.
 CC The invention relates to a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis. Sequences AAY27016-19 represent
 CC specific examples of Apo-2L variants. Note: This sequence is not provided
 CC in the specification. It has been created by modifying the wild-type Apo-
 CC 2L sequence provided in Fig 1A
 XX Sequence 281 AA;
 SQ

Query Match 71.9%; Score 202; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.8e-189;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DSDYDNDPDEESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120
 DB 61 DSDYDNDPDEESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQEEIKENTKN 202
 DB 181 FYIYISQTYFRFQEEIKENTKN 202

RESULT 54
 ABG72257
 ID ABG72257 standard; protein; 281 AA.
 AC ABG72257;
 XX
 DT 04-MAR-2003 (first entry)
 XX Human tumour related apoptosis inducing ligand (Trail).
 DE Human; tumour related apoptosis inducing ligand; Trail;
 KW Trail prokaryotic expression system; tumour cell death.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 217
 FT /note= "Encoded by CTT"
 XX
 XX CN1354183-A.
 XX 19-JUN-2002.
 PD

XX 30-NOV-2001; 2001CN-00132371.
 XX 30-NOV-2001; 2001CN-00132371.
 PR (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
 XX Hu Y, Yao Y;
 XX WPI; 2002-751439/82.
 DR N-PSDB; ABX14391.
 XX Tumor death induction ligand gene, gene expression protein and its
 PT preparation method.
 PS Claim 7; Page 10 (disclosure); 17pp; Chinese.
 XX The present invention relates to the isolation of cDNA encoding human
 CC tumour related apoptosis inducing ligand (Trail), and the Trail protein.
 CC The Trail full length cDNA is cloned, and is utilised to create a Trail
 CC prokaryotic expression system. The full length Trail cDNA is used to
 CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
 CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
 CC expression systems. The prokaryotic expression systems created greatly
 CC increase the expression and quantity of the Trail, Trail109, and Trail114
 CC proteins, and may be useful in a new preparation for killing tumour
 CC cells. The present sequence represents the full length human Trail
 CC protein
 XX Sequence 281 AA;
 SQ

Query Match 70.8%; Score 199; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 3.3e-186;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 QY 61 DSDYDNDPDEESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120
 DB 61 DSDYDNDPDEESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGPQ 120
 QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 DB 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
 QY 181 FYIYISQTYFRFQEEIKEN 199
 DB 181 FYIYISQTYFRFQEEIKEN 199

RESULT 55
 AAU99301
 ID AAU99301 standard; protein; 212 AA.
 AC AAU99301;
 XX
 DT 24-SEP-2002 (first entry)
 XX Human TRAIL splice variant 8, rpl-6-6, protein.
 DE Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
 XX chromosome 3q26; rpl-6-6.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH

XX The invention relates to a cytokine designated as tumour necrosis factor
 CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
 CC of certain target cells, including cancer cells and virally infected
 CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
 CC treating viral infections (e.g. bovine viral diarrhoea or human
 CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
 CC melanoma), as a research reagent useful in studying apoptosis including
 CC the regulation of programmed cell death. TRAIL DNA sequences may be
 CC employed in developing a gene therapy approach to treating disorders
 CC mediated by defective or insufficient amounts of TRAIL, in the production
 CC of TRAIL polypeptides and as probes or primers in polymerase chain
 CC reactions (PCR). The present sequence is growth hormone (GH)-derived
 CC leader peptide-leucine zipper-human TRAIL fusion protein
 XX Sequence 253 AA;

Query Match 66.5%; Score 187; DB 4; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVREGRGQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 154
 DB 67 TSEETISTVQEKQONISPLVREGRGQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 126
 QY 155 ESSRSGHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKT 214
 DB 127 ESSRSGHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKT 186
 QY 215 SYDPDILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 DB 187 SYDPDILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
 QY 275 FGAFVLVG 281
 DB 247 FGAFVLVG 253

RESULT 57
 ABU08564
 ID ABU08564 standard; protein; 253 AA.
 AC ABU08564;
 XX
 XX 05-JUN-2003 (first entry)
 DE Human Growth hormone/leucine zipper/TRAIL 95-281 fusion protein.
 KW Human; TNF related apoptosis inducing ligand; TRAIL;
 KW tumour necrosis factor; apoptosis; haemostatic; immunosuppressive;
 KW anti-inflammatory; dermatological; thrombotic microangiopathy;
 KW thrombotic thrombocytopenic purpura; TTP; HUS; SLE; clotting disorder;
 KW adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;
 KW systemic lupus erythematosus; growth hormone; leucine zipper.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Unidentified.
 XX US521228-B1.
 XX 18-FEB-2003.
 XX 02-APR-2001; 2001US-00825563.
 XX 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 PR 25-JUN-1996; 96US-00670354.
 PR 26-MAR-1998; 98US-00048641.
 PR 10-NOV-1998; 98US-00190046.
 PR 26-MAY-1999; 99US-00320424.
 XX
 PA (IMM) IMMUNEX CORP.

XX Willey SR, Goodwin RG;
 PI
 XX WPI; 2003-340628/32.
 DR N-FSDB; ABX93872.
 XX
 PT Novel antibody which binds to human tumor necrosis factor related
 PT apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated
 PT apoptosis of a target cell, or blocking binding of TRAIL to a target
 PT cell.
 XX
 PS Disclosure; Fig 3; 40pp; English.
 XX
 CC The invention relates to an antibody that specifically binds: (a) the
 CC human tumor necrosis factor (TNF) related apoptosis inducing ligand
 CC (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL
 CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of
 CC ABU08558; or (d) a fragment of the TRAIL protein. Also included is an
 CC antigen-binding fragment of the antibody (a monoclonal antibody), a
 CC hybridoma cell line that produces the antibody. The antibody is used in
 CC assays to detect the presence of TRAIL polypeptides, either in vitro or
 CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of
 CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.
 CC The antibody is useful for treating disorders mediated or exacerbated by
 CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic
 CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)
 CC (even though it can strike children as well) small blood vessel clotting
 CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic
 CC lupus erythematosus (SLE). The present sequence represents a Growth
 CC hormone signal peptide/leucine zipper/TRAIL 95-281 fusion protein
 XX Sequence 253 AA;

Query Match 66.5%; Score 187; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1.7e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVREGRGQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 154
 DB 67 TSEETISTVQEKQONISPLVREGRGQVAAHITGRGRSNTLSSPNSKNEKALGRKINSW 126
 QY 155 ESSRSGHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKT 214
 DB 127 ESSRSGHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKT 186
 QY 215 SYDPDILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 DB 187 SYDPDILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 246
 QY 275 FGAFVLVG 281
 DB 247 FGAFVLVG 253

RESULT 58
 AAEL1038
 ID AAEL1038 standard; protein; 256 AA.
 XX
 XX AAEL1038;
 XX
 XX 18-DEC-2001 (first entry)
 DE CMV-derived leader peptide-leucine zipper-human TRAIL fusion protein.
 KW Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 KW melanoma; cytomegalovirus; CMV; leucine zipper; fusion protein;
 KW chimeric protein.
 XX
 OS Homo sapiens.
 OS Cytomegalovirus.
 OS Unidentified.

OS XX Chimeric.

PH Key Location/Qualifiers

FT Region 1. .29

FT Region 30. .32

FT Region /note= "CMV-derived leader peptide"

FT Region /note= "Tripeptide corresponding to an oligonucleotide employed in vector construction"

FT Region 33. .66

FT Region /note= "Leucine zipper peptide"

FT Region 67. .69

FT Region /note= "Tripeptide corresponding to an oligonucleotide employed in vector construction"

FT Region 70. .256

FT Region /note= "Human TRAIL protein fragment"

XX US6284236-B1.

XX 04-SEP-2001.

XX 26-MAY-1999; 99US-00320424.

XX 29-JUN-1995; 95US-00496632.

XX 01-NOV-1995; 95US-00548368.

XX 25-JUN-1996; 96US-00670354.

XX 26-MAR-1998; 98US-00048641.

XX 10-NOV-1998; 98US-00190046.

XX (IMMV) IMMUNEX CORP.

XX Wiley SR, Goodwin RG;

XX WPI; 2001-595463/67.

XX N-PSDB; AAD18399.

XX New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhoea or lymphoma). immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).

XX Claim 20; Fig 4; 41pp; English.

XX The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is a DNA encoding cytomegalovirus (CMV)-derived leader peptide-leucine zipper-human TRAIL fusion protein

XX SQ Sequence 256 AA;

Query Match 66.5%; Score 187; DB 4; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.7e-174;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 TSETISTVQKQNIPLVREGRQVAAHITGRGRNTLSSPNSKNEKALGRKINSW 154

Db 70 TSETISTVQKQNIPLVREGRQVAAHITGRGRNTLSSPNSKNEKALGRKINSW 129

Qy 155 ESSRSGHSFLNLHRLNGELVIEHKGFFYYISQTYFRQBEIKENTKDKQWQYIYKYT 214

Db 130 ESSRSGHSFLNLHRLNGELVIEHKGFFYYISQTYFRQBEIKENTKDKQWQYIYKYT 189

Qy 215 SYDPDILLMSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLMDHEASF 274

Db 190 SYDPDILLMSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLMDHEASF 249

Qy 275 FGAFPLVG 281

Db 250 FGAFPLVG 256

RESULT 59

ABU08565

ID ABU08565 standard; protein; 256 AA.

XX AC ABU08565;

XX 05-JUN-2003 (first entry)

DT CMV sig. pep./leucine zipper/TRAIL 95-281 fusion protein.

DE Human; TNF related apoptosis inducing ligand; TRAIL; CMV;

XX tumour necrosis factor; apoptosis; haemostatic; immunosuppressive;

XX antiinflammatory; dermatological; thrombotic microangiopathy;

XX thrombotic thrombocytopenic purpura; TTP; HUS; SLE; clotting disorder;

XX adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;

XX systemic lupus erythematosus; leucine zipper.

XX Homo sapiens.

OS Human Cytomegalovirus.

OS Unidentified.

OS Chimeric.

XX US6521228-B1.

XX 18-FEB-2003.

XX 02-APR-2001; 2001US-00825563.

XX 29-JUN-1995; 95US-00496632.

XX 01-NOV-1995; 95US-00548368.

XX 25-JUN-1996; 96US-00670354.

XX 26-MAR-1998; 98US-00048641.

XX 10-NOV-1998; 98US-00190046.

XX 26-MAY-1999; 99US-00320424.

XX (IMMV) IMMUNEX CORP.

XX Wiley SR, Goodwin RG;

XX WPI; 2003-340628/32.

XX N-PSDB; ABX3873.

XX Novel antibody which binds to human tumor necrosis factor related apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated apoptosis of a target cell, or blocking binding of TRAIL to a target cell.

XX Disclosure; Fig 4; 40pp; English.

XX The invention relates to an antibody that specifically binds: (a) the human tumor necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL polypeptide; (c) a polypeptide comprising amino acids 124-276 of ABU08558, or (d) a fragment of the TRAIL protein. Also included is an antigen-binding fragment of the antibody (a monoclonal antibody), a hybridoma cell line that produces the antibody. The antibody is used in assays to detect the presence of TRAIL polypeptides. The antibody is used in vivo, to target cells by affinity chromatography, blocking binding of TRAIL to target cells and thus inhibiting a biological activity of TRAIL. The antibody is useful for treating disorders mediated or exacerbated by TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS) even though it can strike children as well) small blood vessel clotting disorders e.g., cardiac problems in paediatric AIDS patients and systemic lupus erythematosus (SLE). The present sequence represents a CMV (human cytomegalovirus) signal peptide/leucine zipper/TRAIL 95-281 fusion protein


```

SQ      Sequence 256 AA;
Query Match      66.5%; Score 187; DB 6; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.7e-174;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      95 TSEETISTVQEKQONISPLVRERGPORVAAHITGRGRNTLSSPNSKNEKALGRKINSW 154
Db      70 TSEETISTVQEKQONISPLVRERGPORVAAHITGRGRNTLSSPNSKNEKALGRKINSW 129
QY      155 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 214
Db      130 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 189
QY      215 SYDPDILLMKSRNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db      190 SYDPDILLMKSRNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 249
QY      275 FGAFVLVG 281
Db      250 FGAFVLVG 256

RESULT 60
AA017496
ID      AA017496 standard; protein; 461 AA.
AC      AA017496;
DT      11-JUL-2002 (first entry)
DE      Antibody-cytokine fusion protein #3.
KW      Antibody-cytokine fusion protein; proapoptotic; immunomodulatory; cancer;
KW      immune disease; multiple sclerosis; rheumatoid arthritis; cytostatic;
KW      antiinflammatory; antirheumatic; antiarthritic; antibacterial; virucide;
KW      protozoacide; antiallergic; antidiabetic; diabetes; infection;
KW      inflammation.
OS      Synthetic.
FX      Key      Location/Qualifiers
FH      Peptide      1..19
FT      Region      /note= "signal peptide"
FT      Region      /note= "ScFv antibody fragment"
FT      Region      /note= "linker peptide"
FT      Region      /note= "linker peptide"
FT      Region      /note= "immunoglobulin CH3 domain"
FT      Region      /note= "linker peptide"
FT      Region      /note= "linker peptide"
FT      Region      /note= "human TRAIL protein fragment"
PN      WO200222680-A2.
XX      21-MAR-2002.
PF      07-SEP-2001; 2001WO-EP010364.
PR      15-SEP-2000; 2000DE-01045591.
PA      (PFIZ/) PFIZENWATER K.
PA      (WAJA/) WAJANT H.
XX      Pfizenmaier K, Wajant H, Moosmayer D, Wuest T;
XX      WPI; 2002-362336/39.
DR      N-PSDB; AAL46272.
XX      New polypeptide prodrug, useful e.g. for treating tumors, comprises
PT      cytokine, oligomerization domain and antibody specific for cytokine

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PT      receptor.
XX      Disclosure; Page 38-39; 45pp; German.
CC      The present invention relates to proteins comprising a segment with
CC      biological activity for a specific target molecule, a peptide linker, and
CC      a segment that is an antibody (or fragment) that recognises a specific
CC      target molecule on a cell surface. In absence of site-specific and/or
CC      selective binding of the antibody to the target, the biologically active
CC      segment has no biological activity. The proteins are useful in the
CC      treatment of cancers, infections (bacterial, viral or protozoal),
CC      metabolic diseases, inflammatory states (including allergy and transplant
CC      rejection), and autoimmune diseases, especially rheumatic/arthritis
CC      diseases but also multiple sclerosis and diabetes. The present sequence
CC      is a fusion protein of the invention
XX      SQ      Sequence 461 AA;

Query Match      66.5%; Score 187; DB 5; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.7e-174;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      95 TSEETISTVQEKQONISPLVRERGPORVAAHITGRGRNTLSSPNSKNEKALGRKINSW 154
Db      275 TSEETISTVQEKQONISPLVRERGPORVAAHITGRGRNTLSSPNSKNEKALGRKINSW 334
QY      155 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 214
Db      335 ESSRSCHSFLSNLHNLNGELVHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYT 394
QY      215 SYDPDILLMKSRNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db      395 SYDPDILLMKSRNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 454
QY      275 FGAFVLVG 281
Db      455 FGAFVLVG 461

RESULT 61
AA017495
ID      AA017495 standard; protein; 480 AA.
AC      AA017495;
DT      11-JUL-2002 (first entry)
DE      Antibody-cytokine fusion protein #2.
KW      Antibody-cytokine fusion protein; proapoptotic; immunomodulatory; cancer;
KW      immune disease; multiple sclerosis; rheumatoid arthritis; cytostatic;
KW      antiinflammatory; antirheumatic; antiarthritic; antibacterial; virucide;
KW      protozoacide; antiallergic; antidiabetic; diabetes; infection;
KW      inflammation.
OS      Synthetic.
FX      Key      Location/Qualifiers
FH      Peptide      1..19
FT      Region      /note= "signal peptide"
FT      Region      /note= "ScFv antibody fragment"
FT      Region      /note= "linker peptide"
FT      Region      /note= "linker peptide"
FT      Region      /note= "human TRAIL protein fragment"
PN      WO200222680-A2.
XX      21-MAR-2002.
PF      07-SEP-2001; 2001WO-EP010364.
PR      15-SEP-2000; 2000DE-01045591.
PA      (PFIZ/) PFIZENWATER K.
PA      (WAJA/) WAJANT H.
XX      Pfizenmaier K, Wajant H, Moosmayer D, Wuest T;
XX      WPI; 2002-362336/39.
DR      N-PSDB; AAL46272.
XX      New polypeptide prodrug, useful e.g. for treating tumors, comprises
PT      cytokine, oligomerization domain and antibody specific for cytokine

```

PR 15-SEP-2000; 2000DE-01045591.
 XX (PFIZ/) PFIZENMAIER K.
 PA (WAJA/) WAJANT H.
 XX Pfizenmaier K, Wajant H, Moosmayer D, Wuest T;
 XX WPI; 2002-362336/39.
 DR N-PSDB; AAL46271.
 XX
 PT New polypeptide prodrug, useful e.g. for treating tumors, comprises
 PT cytokine, oligomerization domain and antibody specific for cytokine
 PT receptor.
 XX
 PS Disclosure; Page 36-37; 45pp; German.
 XX
 CC The present invention relates to proteins comprising a segment with
 CC biological activity for a specific target molecule, a peptide linker, and
 CC a segment that is an antibody (or fragment) that recognises a specific
 CC target molecule on a cell surface. In absence of site-specific and/or
 CC selective binding of the antibody to the target, the biologically active
 CC segment has no biological activity. The proteins are useful in the
 CC treatment of cancers, infections (bacterial, viral or protozoal),
 CC metabolic diseases, inflammatory states (including allergy and transplant
 CC rejection), and autoimmune diseases, especially rheumatic/arthritis
 CC diseases but also multiple sclerosis and diabetes. The present sequence
 CC is a fusion protein of the invention
 XX
 SQ Sequence 480 AA;

Query Match 66.5%; Score 187; DB 5; Length 480;
 Best Local Similarity 100.0%; Pred. No. 2.8e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 95 TSEETISTVQEKQONISPLVREGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSW 154
 Db 294 TSEETISTVQEKQONISPLVREGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSW 353
 QY 155 ESSRSGHSFSLNHLRNGELVHKEGFIYYSQTYFRFOEIKENTKDKQWQYIYKYT 214
 Db 354 ESSRSGHSFSLNHLRNGELVHKEGFIYYSQTYFRFOEIKENTKDKQWQYIYKYT 413
 QY 215 SYDPDILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 Db 414 SYDPDILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 473
 QY 275 FGAFLVG 281
 Db 474 FGAFLVG 480

RESULT 62
 ID AAO17494
 AC AAO17494 standard; protein; 614 AA.
 AC AAO17494;
 DT 11-JUL-2002 (first entry)
 XX Antibody-cytokine fusion protein #1.
 XX
 KW Antibody-cytokine fusion protein; proapoptotic; immunomodulatory; cancer;
 KW immune disease; multiple sclerosis; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antirheumatic; antiarthritic; antibacterial; virucide;
 KW protozoacide; antiallergic; antidiabetic; diabetes; infection;
 XX inflammation.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT 20..274
 FT Region

FT Region /note= "SCFv antibody fragment"
 FT 275..314
 FT /note= "linker peptide"
 FT 315..418
 FT /note= "immunoglobulin CH3 domain"
 FT 419..427
 FT /note= "linker peptide"
 FT 428..614
 FT /note= "human TRAIL protein fragment"
 XX

PN WO200222680-A2.

XX 21-MAR-2002.

PD 07-SEP-2001; 2001WO-EP010364.

XX 15-SEP-2000; 2000DE-01045591.

XX (PFIZ/) PFIZENMAIER K.

PA (WAJA/) WAJANT H.

XX Pfizenmaier K, Wajant H, Moosmayer D, Wuest T;

XX WPI; 2002-362336/39.

DR N-PSDB; AAL46270.

XX New polypeptide prodrug, useful e.g. for treating tumors, comprises
 PT cytokine, oligomerization domain and antibody specific for cytokine
 PT receptor.
 XX

PS Disclosure; Page 33-35; 45pp; German.

XX The present invention relates to proteins comprising a segment with
 CC biological activity for a specific target molecule, a peptide linker, and
 CC a segment that is an antibody (or fragment) that recognises a specific
 CC target molecule on a cell surface. In absence of site-specific and/or
 CC selective binding of the antibody to the target, the biologically active
 CC segment has no biological activity. The proteins are useful in the
 CC treatment of cancers, infections (bacterial, viral or protozoal),
 CC metabolic diseases, inflammatory states (including allergy and transplant
 CC rejection), and autoimmune diseases, especially rheumatic/arthritis
 CC diseases but also multiple sclerosis and diabetes. The present sequence
 CC is a fusion protein of the invention
 XX
 SQ Sequence 614 AA;

Query Match 66.5%; Score 187; DB 5; Length 614;
 Best Local Similarity 100.0%; Pred. No. 3.5e-174;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 TSEETISTVQEKQONISPLVREGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSW 154
 Db 428 TSEETISTVQEKQONISPLVREGPQVAAHITGTRGNTLSSPNSKNEKALGRKINSW 487
 QY 155 ESSRSGHSFSLNHLRNGELVHKEGFIYYSQTYFRFOEIKENTKDKQWQYIYKYT 214
 Db 488 ESSRSGHSFSLNHLRNGELVHKEGFIYYSQTYFRFOEIKENTKDKQWQYIYKYT 547
 QY 215 SYDPDILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
 Db 548 SYDPDILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASF 607
 QY 275 FGAFLVG 281
 Db 608 FGAFLVG 614

RESULT 63
 AAB28692
 ID AAB28692 standard; protein; 441 AA.
 XX
 AC AAB28692;
 XX

DT 14-FEB-2001 (first entry)
DE FC-huAGP-1 (95-281) fusion protein.
XX Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
XX anti-inflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW transplant rejection; cardiovascular disease; arteriosclerosis;
KW FC-huAGP-1; fusion protein.
XX Homo sapiens.
OS WO200063253-A1.
FN 26-OCT-2000.
XX 24-MAR-2000; 2000WO-US008004.
XX 16-APR-1999; 99US-00293245.
XX (AMGE-) AMGEN INC.
XX Hsu H, Meng S;
XX WPI: 2000-665240/64.
DR N-PSDB; AAC67832.
XX Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
PI Disclosure; Fig 3; 93pp; English.
XX The present sequence is an AGP-1 fusion protein. AGP-1 is a type II
CC transmembrane protein. The fusion proteins comprise an Fc immunoglobulin
CC region fused to the N-terminal portion of the AGP-1 protein. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC proteins have increased biological activity compared to the soluble AGP-1
CC proteins used in prior art therapies
XX Sequence 441 AA;
SQ
Query Match 66.2%; Score 186; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.5e-173; Indels 0; Gaps 0;
Matches 186; Conservative 0; Mismatches 0;
QY 95 TSEETISTVQEQKQNISPLVRRGQPVAAHITGTRGRSNTLSSPNSKNEALGRKINSW 154
Db |||||||
QY 256 TSEETISTVQEQKQNISPLVRRGQPVAAHITGTRGRSNTLSSPNSKNEALGRKINSW 315
Db |||||||
QY 155 ESSRSGHFLSNLHUNGELVHEKGFYIYSQTYFRQEEIKENTKDKQMVYIYKT 214
Db |||||||
QY 316 ESSRSGHFLSNLHUNGELVHEKGFYIYSQTYFRQEEIKENTKDKQMVYIYKT 375
Db |||||||
QY 215 SYDPDILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 274
Db |||||||
QY 376 SYDPDILLMKARSNCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASF 435
Db |||||||
QY 275 FGAFLV 280
Db |||||||
QY 436 FGAFLV 441
Db |||||||
RESULT 64
ADB61476
ID ADB61476 standard; protein; 281 AA.
XX

AC ADB61476;
XX 04-DEC-2003 (first entry)
XX Human Apo-2 ligand protein mutant S96C.
DE Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
XX high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW human; mutant; mutein.
XX Synthetic.
OS Homo sapiens.
FN Key Location/Qualifiers
XX Misc-difference 96 /note= "Native residue of Ser is substituted by Cys"
FT WO2003029420-A2.
XX 10-APR-2003.
XX 01-OCT-2002; 2002WO-US031210.
XX 02-OCT-2001; 2001US-032622P.
XX (GETH) GENENTECH INC.
XX Kelley RF, Lindstrom SH;
XX WPI: 2003-541400/51.
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
PT cancer or an immune-related disease such as multiple sclerosis, comprises
PT amino acid substitutions in the native sequence of the Apo-2 ligand.
XX Claim 1; Page; 92pp; English.
XX The invention relates to a novel isolated Apo-2 ligand variant
CC polypeptide having a sequence that differs from the native sequence
CC having 281 amino acids given in specification. The Apo-2 ligand variant
CC polypeptide is selected from a polypeptide having substitutions at
CC residue positions identified from x-ray crystal structure of the
CC DR5.Apo2L complex. The polypeptide having the substitutions made at
CC residue position(s) selected from 20 positions such as S96C, S101C,
CC S111C, V114C, R115C, E116C, N134C, N140C, N144C, N152C, S153C, R170C,
CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the human Apo-2 ligand mutant S96C
CC protein of the invention. NOTE: This sequence is not shown in the
CC specification. It has been created from information provided in claim 1
CC and from the sequence in Fig 1 of the specification.
XX Sequence 281 AA;
SQ
Query Match 65.8%; Score 185; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.7e-172;

Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 EETISTVQEQKQNTISPLVRRGPGORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWES 156
 |||||
 Db 97 EETISTVQEQKQNTISPLVRRGPGORVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWES 156
 |||||

QY 157 SRSGHSLNHLRANGELVTHEKGFYIYSQTVFRFOEEIKENTQNDKQWQVYIKYTSY 216
 |||||
 Db 157 SRSGHSLNHLRANGELVTHEKGFYIYSQTVFRFOEEIKENTQNDKQWQVYIKYTSY 216
 |||||

QY 217 PDPILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLMDHDEASFFG 276
 |||||
 Db 217 PDPILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFVSVTNEHLMDHDEASFFG 276
 |||||

QY 277 AFLVG 281
 |||||
 Db 277 AFLVG 281
 |||||

RESULT 65
 ADB61480
 ID ADB61480 standard; protein; 281 AA.
 XX AC ADB61480;
 XX

DT 04-DEC-2003 (first entry)
 XX DE Human Apo-2 ligand protein mutant R115C.
 XX

KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX OS Synthetic.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Misc-difference 115 /note= "Native residue of Arg is substituted by Cys"
 FT

PN W02003029420-A2.
 XX 10-APR-2003.
 XX 01-OCT-2002; 2002WO-US031210.
 XX 02-OCT-2001; 2001US-0326622P.
 XX (GETH) GENENTECH INC.
 XX Kelley RF, Lindstrom SH;
 XX WPI; 2003-541400/51.
 XX

Novel isolated Apo-2 ligand variant polypeptide useful for treating
 cancer or an immune-related disease such as multiple sclerosis, comprises
 amino acid substitutions in the native sequence of the Apo-2 ligand.
 PS Claim 1; Page; 92pp; English.
 XX

The invention relates to a novel isolated Apo-2 ligand variant
 polypeptide having a sequence that differs from the native sequence
 having 281 amino acids given in specification. The Apo-2 ligand variant
 polypeptide is selected from a polypeptide having substitutions at
 residue positions identified from x-ray crystal structure of the
 DR5.Apo2L complex. The polypeptide having the substitutions made at
 residue position(s) selected from 20 positions such as S96C, S101C,
 S111C, R114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
 R170K, R170S, D234C, E249C, R255C, E263C, H264C, such that the
 residue position is, outside of the receptor contact region of the
 DR5.Apo2L complex, and displays high solvent accessibility in the crystal

CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytosolic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant R115C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX

SQ Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVTVYVFTNELKQMDKYSKSGIACFLKE 60
 |||||

QY 61 DSYWDPNDEESNPSQWQKQWLRLVVKMLRTSEETISIVQEQKQNTISPLVRRGPGQ 120
 |||||
 Db 61 DSYWDPNDEESNPSQWQKQWLRLVVKMLRTSEETISIVQEQKQNTISPLVRRGPGQ 120
 |||||

QY 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESRSGHSLNHLRANGELVTHEKG 180
 |||||
 Db 121 RVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESRSGHSLNHLRANGELVTHEKG 180
 |||||

QY 181 FYIYSQTVFRFOEEIKENTQNDKQWQVYIKYTSYDPDPILLMKSARNCSWSDAEGLY 240
 |||||
 Db 181 FYIYSQTVFRFOEEIKENTQNDKQWQVYIKYTSYDPDPILLMKSARNCSWSDAEGLY 240
 |||||

QY 241 SIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAFVLVG 281
 |||||
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAFVLVG 281
 |||||

RESULT 66

ADB61482
 ID ADB61482 standard; protein; 281 AA.
 XX AC ADB61482;
 XX

DT 04-DEC-2003 (first entry)
 XX DE Human Apo-2 ligand protein mutant N134C.
 XX

KW Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX OS Synthetic.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Misc-difference 134 /note= "Native residue of Asn is substituted by Cys"
 FT

PN W02003029420-A2.

XX 10-APR-2003.
 PD

SQ Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNKLKQMDKYSKGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVFTVLLQSLCAVAVYVFTNKLKQMDKYSKGIACFLKE 60

QY 61 DSDYWDNDESMNSPCWQVKWQLRQLVKMLTSEETISTVQEKQNTISPLVRERGPO 120
 DB 61 DSDYWDNDESMNSPCWQVKWQLRQLVKMLTSEETISTVQEKQNTISPLVRERGPO 120

QY 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 DB 121 RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEVGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 68
 ADB61478
 ID ADB61478 standard; protein; 281 AA.
 AC ADB61478;
 XX 04-DEC-2003 (first entry)
 XX Human Apo-2 ligand protein mutant S111C.
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 XX high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 XX trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 XX lung; breast; immune-related disease; arthritis; multiple sclerosis;
 XX human; mutant; mutein.
 XX Synthetic.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX Misc-difference 111 /note= "Native residue of Ser is substituted by Cys"
 XX W02003029420-A2.
 XX 10-APR-2003.
 XX 01-OCT-2002; 2002WO-US031210.
 XX 02-OCT-2001; 2001US-0326622P.
 XX (GETH) GENENTECH INC.
 XX Kelley RF, Lindstrom SH;
 XX WPI; 2003-541400/51.
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
 XX cancer or an immune-related disease such as multiple sclerosis, comprises
 XX amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX Claim 1; Page; 92pp; English.
 XX The invention relates to a novel isolated Apo-2 ligand variant
 XX polypeptide having a sequence that differs from the native sequence
 XX having 281 amino acids given in specification. The Apo-2 ligand variant

CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, E115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R259C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant S111C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 XX SQ Sequence 281 AA;

FH Key Location/Qualifiers
 FT Misc-difference 116 /note= "Native residue of Glu is substituted by Cys"
 XX WO2003029420-A2.
 XX 10-APR-2003.
 XX 01-OCT-2002; 2002WO-US031210.
 XX 02-OCT-2001; 2001US-0326622P.
 XX (GETH) GENENTECH INC.
 XX Kelley RF, Lindstrom SH;
 XX WPI; 2003-541400/51.
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX Claim 1; Page; 92pp; English.
 XX The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, R179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 XX treating cancer (such as lung, breast, colon or colorectal cancer) or an

Db 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDPDILLMKSRNSCWSKDAEYGLY 240
 Qy 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVVG 281
 RESULT 70
 ADB61487
 ID ADB61487 standard; protein; 281 AA.
 XX ADB61487;
 XX 04-DEC-2003 (first entry)
 XX Human Apo-2 ligand protein mutant R170C.
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 170 /note= "Native residue of Arg is substituted by Cys"
 XX WO2003029420-A2.
 XX 10-APR-2003.
 XX 01-OCT-2002; 2002WO-US031210.
 XX 02-OCT-2001; 2001US-0326622P.
 XX (GETH) GENENTECH INC.
 XX Kelley RF, Lindstrom SH;
 XX WPI; 2003-541400/51.
 XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
 PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX Claim 1; Page; 92pp; English.
 XX The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, R179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKGIACFLKE 60
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATVYVFTNELKQMDKYSKGIACFLKE 60
 Qy 61 DDSYWDPNDESMNSPCQVQWQLRQVLRKMLRTSETISTVQKQNIPLVRERGPQ 120
 Db 61 DDSYWDPNDESMNSPCQVQWQLRQVLRKMLRTSETISTVQKQNIPLVRERGPQ 120
 Qy 121 RVAAHITGRGSRNTLSSPNSKNEALGRKKNWESSRSGHSFSLNLRNGELVIEHKG 180
 Db 121 RVAAHITGRGSRNTLSSPNSKNEALGRKKNWESSRSGHSFSLNLRNGELVIEHKG 180
 Qy 181 FYIYSQTYFRFQBEIKENTKNDKQMVQYIYKTSYDPDILLMKSRNSCWSKDAEYGLY 240

CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant R170C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 SQ Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 71
 ADB61485
 ID ADB61485 standard; protein; 281 AA.
 AC ADB61485;
 XX
 DT 04-DEC-2003 (first entry)
 XX Human Apo-2 ligand protein mutant N152C.
 DE
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 KW high solvent accessibility; cytosolic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 152
 FT /note= "Native residue of Asn is substituted by Cys"
 XX
 PN WO2003029420-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 01-OCT-2002; 2002WO-US031210.
 XX
 PR 02-OCT-2001; 2001US-032622P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Kelley RF, Lindstrom SH;
 XX
 DR WPT; 2003-541400/51.
 XX
 PT Novel isolated Apo-2 ligand variant polypeptide useful for treating

PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.
 XX
 PS Claim 1; Page; 92pp; English.
 XX

CC The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, R114C, R115C, E116C, N134C, N140C, E144C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytosolic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant N152C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.
 XX
 SQ Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120
 DB 61 DDSYWDNDDESMNSPCWQVQWQLRQLVRKMLTSEETISTVQEKQONISPLVRERGQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQWQYIYKYTSYDPPILLMKSARNCSKDAEYGLY 240
 QY 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 72
 ADB61490
 ID ADB61490 standard; protein; 281 AA.
 XX
 AC ADB61490;
 XX
 DT 04-DEC-2003 (first entry)
 XX Human Apo-2 ligand protein mutant K179C.
 DE
 XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;

KW	high solvent accessibility; cytosolic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW	lung; breast; immune-related disease; arthritis; multiple sclerosis; human; mutant; mutein.
XX	Synthetic.
OS	Os sapiens.
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 179
FT	/note= "Native residue of Lys is substituted by Cys"
FT	
PN	WO2003029420-A2.
PN	
PD	10-APR-2003.
XX	
XX	01-OCT-2002; 2002WO-US031210.
XX	
PR	02-OCT-2001; 2001US-0326622P.
XX	
PA	(GETH) GENENTECH INC.
XX	
XX	Kelley RF, Lindstrom SH;
PI	
XX	WPI; 2003-541400/51.
DR	
XX	
CC	Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.
PT	
PT	Claim 1; Page; 92pp; English.
XX	
CC	The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 281 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DR5.Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S96C, S101C, S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C, R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DR5.Apo2L complex, and displays high solvent accessibility in the crystal structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant K179C protein of the invention. NOTE: This sequence is not shown in the specification. It has been created from information provided in claim 1 and from the sequence in Fig 1 of the specification.
XX	
CC	Sequence 281 AA;
XX	
CC	Query Match 64.11%; Score 180; DB 7; Length 281;
XX	Best Local Similarity 99.6%; Pred. No. 1.3e-167;
XX	Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 MAMMEVQGGPSLGQFCVLIVLFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
DB	1 MAMMEVQGGPSLGQFCVLIVLFTVLLQSLCAVATVYVFTNELKOMQDKYSKSGIACFLKE 60
QY	61 DDSYDNDDEESMNSPCWQVKWLQRLVRKMLRSTSETISTVQEQKQNTSPVLRERGPQ 120

CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant S101C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.3e-167;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TVQEKQNI SPLYRERGPQVAAHITGRGSRNTLSSPNKNEKALGRKINSWESSRSH 161
 DB 102 TVQEKQNI SPLYRERGPQVAAHITGRGSRNTLSSPNKNEKALGRKINSWESSRSH 161
 QY 162 SFLSNLHRLNGELVIHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYPPIL 221
 DB 162 SFLSNLHRLNGELVIHEKGFYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYPPIL 221
 QY 222 LMKARNCSWKSQAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFGFLVG 281
 DB 222 LMKARNCSWKSQAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFGFLVG 281

RESULT 74

ADB61479
 ID ADB61479 standard; protein; 281 AA.

XX ADB61479;

DT 04-DEC-2003 (first entry)

XX Human Apo-2 ligand protein mutant V114C.

XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;
 XX high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
 KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
 KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
 KW human; mutant; mutein.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

PH Misc-difference 114 /note= "Native residue of Val is substituted by Cys"

FT WO2003029420-A2.

XX 10-APR-2003.

XX 01-OCT-2002; 2002WO-US031210.

XX 02-OCT-2001; 2001US-0326622P.

XX (GETH) GENENTECH INC.

XX Kelley RF, Lindstrom SH;

XX WPI; 2003-541400/51.

XX Novel isolated Apo-2 ligand variant polypeptide useful for treating

PT cancer or an immune-related disease such as multiple sclerosis, comprises
 PT amino acid substitutions in the native sequence of the Apo-2 ligand.

XX Claim 1; Page; 92pp; English.

XX The invention relates to a novel isolated Apo-2 ligand variant
 CC polypeptide having a sequence that differs from the native sequence
 CC having 281 amino acids given in specification. The Apo-2 ligand variant
 CC polypeptide is selected from a polypeptide having substitutions at
 CC residue positions identified from x-ray crystal structure of the
 CC DR5.Apo2L complex. The polypeptide having the substitutions made at
 CC residue position(s) selected from 20 positions such as S96C, S101C,
 CC S111C, V114C, R115C, E116C, N134C, E144C, N152C, S153C, R170C,
 CC R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the
 CC residue position is, outside of the receptor contact region of the
 CC DR5.Apo2L complex, and displays high solvent accessibility in the crystal
 CC structure of the DR5.Apo2L complex. The Apo-2 ligand variant polypeptide
 CC and further compositions have the following activities: cytostatic,
 CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
 CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
 CC inducing apoptosis in mammalian cells, by exposing mammalian cells
 CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
 CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
 CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
 CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
 CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
 CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
 CC immune-related disease (such as arthritis or multiple sclerosis) in a
 CC mammal, by administering to the mammal an effective amount of the Apo-2
 CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
 CC trimer. This sequence represents the human Apo-2 ligand mutant V114C
 CC protein of the invention. NOTE: This sequence is not shown in the
 CC specification. It has been created from information provided in claim 1
 CC and from the sequence in Fig 1 of the specification.

XX Sequence 281 AA;

Query Match 64.1%; Score 180; DB 7; Length 281;
 Best Local Similarity 99.6%; Pred. No. 1.3e-167;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVYVYFTNELKQMDQKYSKGIACFLKE 60
 DB 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCAVYVYFTNELKQMDQKYSKGIACFLKE 60
 QY 61 DDSYWPNDDEESNNSPCWQVKWQLROLVRKMLRTSEETISTVQEKQNI SPLYRERGPQ 120
 DB 61 DDSYWPNDDEESNNSPCWQVKWQLROLVRKMLRTSEETISTVQEKQNI SPLYRERGPQ 120
 QY 121 RVAAHITGRGSRNTLSSPNKNEKALGRKINSWESSRSHSFLSNLHRLNGELVIHEKG 180
 DB 121 RVAAHITGRGSRNTLSSPNKNEKALGRKINSWESSRSHSFLSNLHRLNGELVIHEKG 180
 QY 181 FYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYPPDILLMKARNCSWKSQAEYGLY 240
 DB 181 FYIYSQYFRFQBEIKENTKNDKQWQYIYKTSYPPDILLMKARNCSWKSQAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGFLVG 281

RESULT 75

ADB61486

ID ADB61486 standard; protein; 281 AA.

XX ADB61486;

XX 04-DEC-2003 (first entry)

XX Human Apo-2 ligand protein mutant S153C.

XX Apo-2 ligand; DR5.Apo2L complex; receptor contact region;

high solvent accessibility; cytosolic; antiarthritic; neuroprotective; trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer; lung; breast; immune-related disease; arthritis; multiple sclerosis; human; mutant; mutagen.

Synthetic.
Homo sapiens.

Key	Location/Qualifiers
-----	---------------------

Misc-difference 153

/note= "Native residue of Ser is substituted by Cys"

WO2003029420-A2.

10-APR-2003

01-OCT-2002: 2002WO-US031210.

02-OCT-2001; 2001US-0326622P.

(GETH) GENENTECH INC.

Kelley RF, Lindstrom SH;

WPI: 2003-541400/51.

Novel isolated Apo-2 ligand variant polypeptide useful for treating cancer or an immune-related disease such as multiple sclerosis, comprises amino acid substitutions in the native sequence of the Apo-2 ligand.

Claim 1: Page: 92pp: English.

The invention relates to a novel isolated Apo-2 ligand variant polypeptide having a sequence that differs from the native sequence having 261 amino acids given in specification. The Apo-2 ligand variant polypeptide is selected from a polypeptide having substitutions at residue positions identified from x-ray crystal structure of the DR5-Apo2L complex. The polypeptide having the substitutions made at residue position(s) selected from 20 positions such as S96C, S101C, S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C, R170K, R170S, K179C, D234C, E249C, R255C, E263C, H264C, such that the residue position is, outside of the receptor contact region of the DR5-Apo2L complex, and displays high solvent accessibility in the crystal structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide and further compositions have the following activities: cytostatic, antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide, an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for inducing apoptosis in mammalian cells, by exposing mammalian cells expressing a receptor selected from DR4 receptor and DR5 receptor to a therapeutically effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide, the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for treating cancer (such as lung, breast, colon or colorectal cancer) or an immune-related disease (such as arthritis or multiple sclerosis) in a mammal, by administering to the mammal an effective amount of the Apo-2 ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand trimer. This sequence represents the human Apo-2 ligand mutant S153C protein of the invention. NOTE: This sequence is not shown in claim 1 and from the sequence in Fig 1 of the specification.

Sequence 281 Å;

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every Match      64.1%; Score 180; DB 7; Length 281;
1st Local Similarity 99.6%; Pred. No. 1.3e-167;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 MAMME'VOGGPSLGQTCVLI VIFTVLLOSLCVAVTYVYFTNELKOMODKYSKSGIACFLKE 60

1 MAMMEVOGGPSLGQTCVLIVIFTVLLOSCLCAVTVVYFTNELKOMODKYSKSGIACFLKE 60

61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

61	DDSYWDPNDESSMPCWVKWQLRQVVRXWILLRTSEETISTVQEQXQINISPLVRRGPQ	120
121	RVAAHITCTGRSNTLSPSPKNEKALGRKINSEWSSRGHGFSLNHLNRNGELVIHEKG	180
121	RVAAHITCTGRSNTLSPSPKNEKALGRKINSEWSSRGHGFSLNHLNRNGELVIHEKG	180
181	FYYIYSQYTFRFOBEIKENTKQWQYIYKYKTSYDPDILLMKSNRSCSKDAEYGLY	240
181	FYYIYSQYTFRFOBEIKENTKQWQYIYKYKTSYDPDILLMKSNRSCSKDAEYGLY	240
241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281
241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG	281

Search completed: March 23, 2004, 09:22:12
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:19:40 ; Search time 45 Seconds
(without alignments)

1970.236 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 281

Sequence: 1 MAMMEVQGPSLQQTCLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	10.3	287	11	Q8K3G0
2	13	4.6	304	13	Q7T1F2
3	8	2.8	465	17	Q9HKC2
4	8	2.8	473	16	Q8FUC2
5	8	2.8	475	10	Q8S6N3
6	8	2.8	643	16	Q9RZ93
7	8	2.8	939	5	Q9NG57
8	8	2.8	950	5	O15788
9	8	2.8	1248	5	Q8IBZ8
10	7	2.5	39	5	Q95NV2
11	7	2.5	73	16	Q7URQ9
12	7	2.5	88	2	Q8KH11
13	7	2.5	92	3	Q870H0
14	7	2.5	93	17	Q9HSN3
15	7	2.5	94	16	Q8PMD7
16	7	2.5	106	10	Q9LV97

17	2.5	107	17	Q97Y77	Q97Y77 sulfolobus
18	2.5	112	16	Q932M3	Q932M3 staphylococ
19	2.5	121	16	Q7U9A5	Q7U9A5 synchococ
20	2.5	125	2	P72087	P72087 neisseria m
21	2.5	134	5	Q8MM82	Q8MM82 caenorhabdi
22	2.5	155	17	Q9YBC2	Q9YBC2 aeropyrum p
23	2.5	157	2	Q83TU1	Q83TU1 staphylococ
24	2.5	172	5	Q9N8D4	Q9N8D4 trypanosoma
25	2.5	193	16	Q8P7K6	Q8P7K6 xanthomonas
26	2.5	204	16	Q82UJ6	Q82UJ6 nitrosomona
27	2.5	216	16	Q8F1X9	Q8F1X9 xanthomonas
28	2.5	217	10	Q8LTD0	Q8LTD0 arabidopsis
29	2.5	220	16	Q89V44	Q89V44 bradyrhizob
30	2.5	222	16	Q8DFN8	Q8DFN8 vibrio vuln
31	2.5	231	5	P90611	P90611 toxoplasma
32	2.5	247	2	Q9EZK4	Q9EZK4 staphylococ
33	2.5	247	16	Q99RD5	Q99RD5 staphylococ
34	2.5	251	3	Q94262	Q94262 schizosacch
35	2.5	253	16	Q98D64	Q98D64 rhizobium l
36	2.5	271	16	Q81WU0	Q81WU0 bacillus an
37	2.5	293	11	Q8ROL0	Q8ROL0 mus musculu
38	2.5	296	16	Q823E7	Q823E7 chlamydophi
39	2.5	298	16	Q8E3I3	Q8E3I3 streptococ
40	2.5	318	4	Q8DXW4	Q8DXW4 streptococ
41	2.5	322	5	Q96QL7	Q96QL7 homo sapien
42	2.5	322	5	Q9VI33	Q9VI33 drosophila
43	2.5	327	16	Q9PEN6	Q9PEN6 xylella fas
44	2.5	329	16	Q9ZKY9	Q9ZKY9 helicobacte
45	2.5	343	16	Q7VUZ3	Q7VUZ3 helicobacte
46	2.5	354	16	Q84846	Q84846 chlamydia t
47	2.5	354	16	Q9FL80	Q9FL80 chlamydia t
48	2.5	359	10	Q9AVE6	Q9AVE6 oryza sativ
49	2.5	361	13	Q98SU0	Q98SU0 xenopus lae
50	2.5	367	5	Q8WPJ2	Q8WPJ2 mytilus edu
51	2.5	374	16	Q7UJW6	Q7UJW6 synchococ
52	2.5	375	16	Q9L5E1	Q9L5E1 salmonella
53	2.5	375	17	Q8TWS8	Q8TWS8 methanopyru
54	2.5	379	16	Q89SW4	Q89SW4 bradyrhizob
55	2.5	389	10	Q9LTH1	Q9LTH1 arabidopsis
56	2.5	401	16	Q9PCZ3	Q9PCZ3 xylella fas
57	2.5	401	16	Q87CC1	Q87CC1 xylella fas
58	2.5	402	4	Q9H766	Q9H766 homo sapien
59	2.5	404	17	Q9UXZ7	Q9UXZ7 sulfolobus
60	2.5	406	16	Q99XN8	Q99XN8 streptococ
61	2.5	406	16	Q8NZ26	Q8NZ26 streptococ
62	2.5	406	16	Q8K5J7	Q8K5J7 streptococ
63	2.5	414	10	Q8S179	Q8S179 oryza sativ
64	2.5	417	2	Q8KIU0	Q8KIU0 pseudomonas
65	2.5	417	2	Q8KIR0	Q8KIR0 pseudomonas
66	2.5	420	5	Q8I514	Q8I514 plasmodium
67	2.5	423	4	Q9NWF0	Q9NWF0 homo sapien
68	2.5	424	10	Q9ZV11	Q9ZV11 arabidopsis
69	2.5	425	10	Q8LP64	Q8LP64 brassica de
70	2.5	427	16	Q83835	Q83835 treponema p
71	2.5	428	17	Q9HSA2	Q9HSA2 halobacteri
72	2.5	429	16	Q9Z913	Q9Z913 chlamydia p
73	2.5	435	11	Q80ZJ8	Q80ZJ8 mus musculu
74	2.5	449	5	Q8SWZ1	Q8SWZ1 drosophila
75	2.5	457	16	Q7WQF5	Q7WQF5 bordetella
76	2.5	457	16	Q7WCF0	Q7WCF0 bordetella
77	2.5	462	12	Q7TBL2	Q7TBL2 bovine ente
78	2.5	462	12	Q7TBK8	Q7TBK8 bovine ente
79	2.5	462	16	Q8EHZ9	Q8EHZ9 shewanella
80	2.5	474	16	Q82GJ4	Q82GJ4 streptomyc
81	2.5	479	16	Q8PDL5	Q8PDL5 xanthomonas
82	2.5	485	5	Q8LIE5	Q8LIE5 plasmodium
83	2.5	494	2	Q8RJJ0	Q8RJJ0 campylobact
84	2.5	494	2	Q8RN10	Q8RN10 campylobact
85	2.5	494	2	Q8RN18	Q8RN18 campylobact
86	2.5	494	2	Q8RN38	Q8RN38 campylobact
87	2.5	494	2	Q8RN13	Q8RN13 campylobact
88	2.5	494	2	Q8RN23	Q8RN23 campylobact
89	2.5	494	2	Q8RJ26	Q8RJ26 campylobact

90 7 2.5 516 11 Q8C4C3 Q8C4C3 mus musculus
 91 7 2.5 519 11 Q8R4G2 Q8R4G2 mus musculus
 92 7 2.5 519 11 Q9JIL4 Q9JIL4 mus musculus
 93 7 2.5 519 11 Q9CQ72 Q9CQ72 mus musculus
 94 7 2.5 523 11 Q8CDP5 Q8CDP5 mus musculus
 95 7 2.5 549 16 Q8PQ15 Q8PQ15 xanthomonas
 96 7 2.5 565 16 Q8KTU6 Q8KTU6 vibrio chol
 97 7 2.5 579 16 Q8RI43 Q8RI43 fusobacteri
 98 7 2.5 630 16 Q8EVS2 Q8EVS2 mycoplasma
 99 7 2.5 680 5 Q8WSN8 Q8WSN8 caenothabdi
 100 7 2.5 686 16 Q8ABC4 Q8ABC4 bacteroides

ALIGNMENTS

RESULT 1
 Q8K3G0 PRELIMINARY; PRT; 287 AA.
 ID Q8K3G0
 AC Q8K3G0
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RA "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A115578; AAM4797.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32979 MW; CA4F5BD7C833FEC CRC64;

Query Match 10.3%; Score 29; DB 11; Length 287;
 Best Local Similarity 100.0%; Pred. No. 1.7e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 KOMVQYVYKYTSYPDILMKARNSCWS 232
 Db |||||

214 KOMVQYVYKYTSYPDILMKARNSCWS 242

RESULT 2
 Q7T1F2 PRELIMINARY; PRT; 304 AA.
 ID Q7T1F2
 AC Q7T1F2
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Tumor necrosis factor related apoptosis inducing ligand.
 GN TRAIL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;
 RA Sayed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;
 RT "Identification and Characterization of Chicken TNF-Superfamily
 RT Ligand 8 (CD30 ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
 RT Inducing Ligand TRAIL).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB114678; BAC79267.1; -.
 SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;
 Query Match 4.6%; Score 13; DB 13; Length 304;
 Best Local Similarity 100.0%; Pred. No. 8.7e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 GFYIYISQTYPRF 192
 Db |||||

184 GFYIYISQTYPRF 196

RESULT 3
 Q8HKC2 PRELIMINARY; PRT; 465 AA.
 ID Q8HKC2
 AC Q8HKC2
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical membrane protein.
 GN TA0679.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=23303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 RT acidophilum.";
 RL Nature 407:508-513 (2000).
 DR EMBL; AL445065; CAC11817.1; -.
 DR InterPro; IPR007272; DUF395.
 DR Pfam; PF04143; DUF395; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 465 AA; 51450 MW; 74E47FAFF0C44B5A CRC64;

Query Match 2.8%; Score 8; DB 17; Length 465;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 SFFGAFVLV 280
 Db |||||

402 SFFGAFVLV 409

RESULT 4
 Q8FUC2 PRELIMINARY; PRT; 473 AA.
 ID Q8FUC2
 AC Q8FUC2
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 GN CE0098
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
 RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

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RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005214; BAC16908.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 473 AA; 52745 MW; 9BFF6D8D8AABE249 CRC64;

Query Match          2.8%; Score 8; DB 16; Length 473;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 LVRRGPQ 120
Db 366 LVRRGPQ 373

RESULT 5
Q8S6N3 PRELIMINARY; PRT; 475 AA.
AC Q8S6N3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative kelch-containing protein.
GN OSUNBA0073L01.3.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Taitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J.J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RA "Oryza sativa chromosome 10 BAC OSUNBA0073L01 genomic sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569 (2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092548; AAM18732.1; -.
DR EMBL; AE017083; AAP53323.1; -.
DR Gramene; Q8S6N3; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006652; Kelch_rep.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01344; Kelch; 2.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00612; Kelch; 2.
DR PROSITE; PS0181; FBOX; 1.
SQ SEQUENCE 475 AA; 51606 MW; 84258271A075D2EE CRC64;

Query Match          2.8%; Score 8; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 LSSPNSKN 143
Db 5 LSSPNSKN 12

RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RT "Polymorphisms in the genes are linked to Chloroquine-Resistant

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RESULT 6
Q9R293 PRELIMINARY; PRT; 643 AA.
AC Q9R293;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Drug transport protein, putative.
GN DRA0061.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577 (1999).
DR EMBL; AE001862; AAP12254.1; -.
DR FIR; G75599; G75599.
DR TIGR; DRA0061; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0015520; F: tetracycline:hydrogen antiporter activity; IEA.
DR GO; GO:0005215; F: transporter activity; IEA.
DR GO; GO:0015904; P: tetracycline transport; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004638; Biflux_EmrB.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR InterPro; IPR001958; TCR_TetA.
DR InterPro; IPR001411; TCR_TetB.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PRO1035; TCR_TETB.
DR PRINTS; PRO1036; TCR_TETB.
DR TIGRFAMS; TIGR00711; efflux_EmrB; 1.
DR PROSITE; PS00850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 643 AA; 67778 MW; 4168A0998E467A63 CRC64;

Query Match          2.8%; Score 8; DB 16; Length 643;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 VLIIVFTV 24
Db 231 VLIIVFTV 238

RESULT 7
Q9NG57 PRELIMINARY; PRT; 939 AA.
AC Q9NG57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CGI protein.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FCCL/HN;
RA Ma C.L., Yu X.B., Shan Z.X., Li X.R.;
RT "Polymorphisms in the genes are linked to Chloroquine-Resistant

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RT Plasmodium falciparum in China.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF260819; AAF69519.1; --
 DR InterPro: IPR009011; Man_6_P_R_bind.
 SQ SEQUENCE 939 AA; 109367 MW; EE96972DC096412D CRC64;

Query Match 2.8%; Score 8; DB 5; Length 939;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
 DB 373 SNTLSSPN 380

RESULT 8

ID O15788 PRELIMINARY; PRT; 950 AA.
 AC O15788;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CGL.
 GN CGL.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1] _SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB3;
 RX MEDLINE=98054002; PubMed=9393853;
 RA Su X., Kirkman L.A., Fujioka H., Wellens T.E.;
 RT "Complex polymorphisms in an approximately kDa protein are linked to
 RT chloroquine-resistant P. falciparum in Southeast Asia and Africa.";
 RL Cell 91:593-603 (1997).
 DR EMBL: AF030690; AAC47851.1; --
 DR FIK; T09076; T09076.
 DR InterPro: IPR009011; Man_6_P_R_bind.
 SQ SEQUENCE 950 AA; 110601 MW; ED19FEA3B517A378 CRC64;

Query Match 2.8%; Score 8; DB 5; Length 950;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
 DB 361 SNTLSSPN 368

RESULT 9

ID Q8IBZ8 PRELIMINARY; PRT; 1248 AA.
 AC Q8IBZ8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cg1 protein.
 GN PF07_0035.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
 RA Quail M., Barrell B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL844506; CAD50843.1; --
 SQ SEQUENCE 1248 AA; 146629 MW; FDBE0EBF1DF769C2 CRC64;

Query Match 2.8%; Score 8; DB 5; Length 1248;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 SNTLSSPN 140
 DB 670 SNTLSSPN 677

RESULT 10

ID Q95NV2 PRELIMINARY; PRT; 39 AA.
 AC Q95NV2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE GM03003p (GM01206p).
 GN BCDNA:GM01206 OR BCDNA:GM03003.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1] _SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060851; AAL28399.1; --
 DR EMBL: AY060825; AAL28373.1; --
 DR FlyBase; FBgn0047295; BCDNA:GM01206.
 SQ SEQUENCE 39 AA; 4446 MW; 432F8F340E895DC6 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 39;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TVLLQSL 29
 DB 25 TVLLQSL 31

RESULT 11

ID Q7URQ9 PRELIMINARY; PRT; 73 AA.
 AC Q7URQ9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB5505.
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Firellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Firellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL: BX294142; CAD74279.1; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 73 AA; 8265 MW; EF2C586B58E7443F CRC64;

Query Match 2.5%; Score 7; DB 16; Length 73;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 MKSARNS 229

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Db          1 MKSARNS 7

RESULT 12
Q8KH11      PRELIMINARY;      PRT;      88 AA.
AC Q8KH11;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Conserved hypothetical membrane protein.
GN PF0795.
OS Bacillus thuringiensis (subsp. israelensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]
RP SEQUENCE FROM N.A.
RA Berry C., O'Neil S., Ben-Dov E., Jones A.F., Murphy L., Quail M.A.,
RA Harris D., Zaritsky A., Parkhill J.;
RT "The complete sequence and organisation of pBtoxis, the toxin-coding
RT plasmid of Bacillus thuringiensis subsp. israelensis";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF731825; CAD30135.1; -.
KW Hypothetical protein.
SQ SEQUENCE 88 AA; 10480 MW; 545BF036F697398 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLRQLVR 89
Db 19 QLRQLVR 25

RESULT 13
Q870H0      PRELIMINARY;      PRT;      92 AA.
AC Q870H0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sun4p (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Z., Dietrich F.S.;
RT "YNL066W(SUN4) mRNA";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY245796; AAP04346.1; -.
FT NON TER 92
SQ SEQUENCE 92 AA; 9444 MW; 6AA4C3BE7C157567 CRC64;

Query Match      2.5%; Score 7; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 VAVTVVY 37
Db 47 VAVTVVY 53

RESULT 14
Q9HSN3      PRELIMINARY;      PRT;      93 AA.
AC Q9HSN3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vag0151C.
GN VAG0151C.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Laeky S.R., Baliga N.S., Thorsson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leithauser B., Kellier K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jabloncki P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlchroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE004981; AAG18770.1; -.
DR PIR; F84175; F84175.
KW Complete proteome.
SQ SEQUENCE 93 AA; 9680 MW; AE96B8359F340B49 CRC64;

Query Match      2.5%; Score 7; DB 17; Length 93;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 FVSVTNE 263
Db 13 FVSVTNE 19

RESULT 15
Q8PMD7      PRELIMINARY;      PRT;      94 AA.
AC Q8PMD7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC1492.
GN XAC1492.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92825;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=306 / ATCC 13902 / XV 101;
RC MEDLINE=22022145; PubMed=12024217;
RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Chapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fomighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locall E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE011781; AAM36362.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 94 AA; 11253 MW; A54AD81C115FBF2B CRC64;

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Query Match          2.5%; Score 7; DB 16; Length 94;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 NDRIFVS 259
DB 65 NDRIFVS 71
|||||

RESULT 16
Q9LV97          PRELIMINARY; PRT; 106 AA.
AC Q9LV97;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Genomic DNA, chromosome 5, Pl clone:MXK3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]_TaxID=3702;
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
DR EMBL; AB019236; BAA97292.1; -.
SQ SEQUENCE 106 AA; 12377 MW; A85ECD52EF507B4C CRC64;

Query Match          2.5%; Score 7; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 IVIFTVL 25
DB 17 IVIFTVL 23
|||||

RESULT 17
Q97Y77          PRELIMINARY; PRT; 107 AA.
AC Q97Y77;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SS01462.
GN SS01462.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]_TaxID=2287;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweez M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
RL EMBL; AB006762; AAK41690.1; -.
DR PIR; C90304; C90304.
DR InterPro; IPR007272; DUF395.

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DR Pfam; PF04143; DUF395; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 107 AA; 12018 MW; 9471937E9819A836 CRC64;

Query Match          2.5%; Score 7; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 PFGAPLV 280
DB 46 PFGAPLV 52
|||||

RESULT 18
Q332M3          PRELIMINARY; PRT; 112 AA.
ID Q332M3
AC Q332M3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated resolvase.
GN TRUNCATED-RES OR SAVP030.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OG Plasmid VRSAp.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]_TaxID=158878;
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanchisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
Lancet 357:1225-1240(2001).
RL EMBL; AP003367; BAB47538.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0000150; F:recombinase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR006118; Recombinase.
DR InterPro; IPR006119; resolvase_N.
DR Pfam; PF00239; resolvase_1.
DR PROSITE; PS00397; RECOMBINASES_1; 1.
DR PROSITE; PS00398; RECOMBINASES_2; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 112 AA; 12884 MW; 1ABB806BBAEDF522 CRC64;

Query Match          2.5%; Score 7; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 FTVLLQS 28
DB 106 FTVLLQS 112
|||||

RESULT 19
Q7U9A5          PRELIMINARY; PRT; 121 AA.
ID Q7U9A5
AC Q7U9A5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical.
GN SYN00353.
OS Synecococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=84588;
RN [1]_TaxID=84588;

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RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Brahamsa B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarran J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.,
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569689; CAE06868.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 121 AA; 13842 MW; CE9C32B4C63811F5 CRC64;

Query Match      2.5%; Score 7; DB 16; Length 121;
Best Local Similarity 100.0%; Pred.No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 QRVAAHI 126
Db 76 QRVAAHI 82
|||||

RESULT 20
P72087 PRELIMINARY; PRT; 125 AA.
AC P72087;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Hemolysin A homolog (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491;
RX MEDLINE=97008141; PubMed=8855317;
RA Tinsley C.R., Nassif X.;
RT "Analysis of the genetic differences between Neisseria meningitidis
RT and Neisseria gonorrhoeae: Two closely related bacteria expressing two
RT different pathogenicities.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:11109-11114(1996).
DR EMBL; U56741; AAC44481.1; -.
FT NON TER 1
FT NON TER 125
FT NON TER 125
SQ SEQUENCE 125 AA; 12834 MW; 92D8F57FD4493496 CRC64;

Query Match      2.5%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred.No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 AAHITGT 129
Db 18 AAHITGT 24
|||||

RESULT 21
Q8MM82 PRELIMINARY; PRT; 134 AA.
AC Q8MM82;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE T02C12.4 protein.
GN T02C12.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
[2]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z38112; CAD36484.1; -.
DR EMBL; Z35603; CAD36484.1; JOINED.
DR EMBL; Z35603; CAD36496.1; -.
DR EMBL; Z38112; CAD36496.1; JOINED.
DR WormPep; T02C12.4; CE30825.
SQ SEQUENCE 134 AA; 15340 MW; 1DB9A0AD8814E477 CRC64;

Query Match      2.5%; Score 7; DB 5; Length 134;
Best Local Similarity 100.0%; Pred.No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 EYGLYSI 242
Db 81 EYGLYSI 87
|||||

RESULT 22
Q9YBC2 PRELIMINARY; PRT; 155 AA.
AC Q9YBC2;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein APE1675.
GN APE1675.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000082; BAA80676.1; -.
DR FIR; G72548; G72548.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 155 AA; 16841 MW; 1AA47C685D52939B CRC64;

Query Match      2.5%; Score 7; DB 17; Length 155;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TLSSPNS 141
Db 88 TLSSPNS 94
|||||

RESULT 23
Q83TU1 PRELIMINARY; PRT; 157 AA.
AC Q83TU1;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

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DE Hypothetical protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Newman, and ISP479C;
RA Steinhuber A., Goerke C., Bayer M.G., Doring G., Wolz C.;
RT "Molecular architecture of the regulatory locus sae of Staphylococcus
aureus and its impact on the expression of virulence factors."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ556794; CAD89109.1; -
DR EMBL; AJ556795; CAD89113.1; -
KW Hypothetical protein.
SQ SEQUENCE 157 AA; 17665 MW; AF973D8D95D5963E CRC64;
Query Match 2.5%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 272 ASFFGAF 278
Db 90 ASFFGAF 96
|||||
RESULT 24
Q9N8D4 PRELIMINARY; PRT; 172 AA.
AC Q9N8D4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acetyltransferase, possible.
GN TB927.1.4490.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Berriman M., Lennard N.J., Harris B.R., Gerrard C.S.,
RA Atkin R.J., Barron A.J., Bart-Delabesse E.N., Bowman S.,
RA Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
RA Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper D.A.,
RA Hertz-Fowler C., Kay M.P., Leech V., Mayes R., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Saese J., Sharp S., Showkhen R.,
RA Gull K., Barrell B.G., Melville S.E.;
RT "The sequence and analysis of the highly polymorphic chromosome I of
the African trypanosome, Trypanosoma brucei."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL929607; CAB95609.1; -
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf; 1.
KW Transferase.
SQ SEQUENCE 172 AA; 19682 MW; B5DD1A59A77E2AB9 CRC64;
Query Match 2.5%; Score 7; DB 5; Length 172;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 140 NSKNEA 146
Db 142 NSKNEA 148
|||||
RESULT 25
Q8P7K6 PRELIMINARY; PRT; 193 AA.
AC Q8P7K6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein XCC2605.
GN XCC2605.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Forghieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities."
RL Nature 417:459-463 (2002).
DR EMBL; AE012372; RAM41877.1; -
DR InterPro; IPR006839; DUF615.
DR InterPro; IPR001232; Skp1.
DR InterPro; IPR008945; Skp1_Skp2.
DR Pfam; PF04751; DUF615; 1.
DR PIRSF; PIRSF016183; UCP016183; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 193 AA; 22001 MW; F00A357929414027 CRC64;
Query Match 2.5%; Score 7; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 QLRQLVR 89
Db 138 QLRQLVR 144
|||||
RESULT 26
Q82JU6 PRELIMINARY; PRT; 204 AA.
AC Q82JU6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LipB; lipote-protein ligase B (EC 6.---).
GN LipB OR NEI488.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773 (2003).
DR EMBL; BX321861; CAD85399.1; -
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0009107; P:lipote biosynthesis; IEA.

DR GO: GO:0006464; P:protein modification; IEA.

DR InterPro: IPR004143; BPL LipA LipB.

DR InterPro: IPR000544; Lipoate_B.

DR Pfam: PF03099; BPL LipA LipB; 1.

DR ProDom: PD006086; Lipoate_B; 1.

DR TIGRFAMs: TIGR00214; LipB; 1.

DR PROSITE: PS01313; LipB; 1.

KW Ligase; Complete proteome.

SQ SEQUENCE 204 AA; 22764 MW; A83F6EF5F0346E61 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 204;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 QQLVRKM 91

Db 97 QQLVRKM 103

RESULT 27

Q8PIX9 PRELIMINARY; PRT; 216 AA.

AC Q8PIX9

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Hypothetical protein XAC2766.

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=306 / ATCC 13902 / XV 101;

RE MEDLINE=2202145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reilbach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities";

RL Nature 417:459-463(2002).

DR EMEL; AB011917; AM37611.1; --

DR InterPro: IPR006839; DUF615.

DR InterPro: IPR001232; Skp1.

DR Pfam: PF04751; DUF615; 1.

DR PIRSF: PIRSF016183; UCP016183; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 216 AA; 24794 MW; 6369B7E20D25B8A CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 QLQLVR 89

Db 161 QLQLVR 167

RESULT 28

Q9LTD0

AC Q9LTD0 PRELIMINARY; PRT; 217 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE HR-like lesion-inducing protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RE MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty Pl and TAC

RT clones";

RL DNA Res. 7:131-135(2000).

DR EMBL; AB025608; BAA95731.1; --

DR InterPro: IPR008637; HR_lesion.

DR Pfam; PF05514; HR_lesion; 1.

DR PFam; PF05514; HR_lesion; 1.

SQ SEQUENCE 217 AA; 25219 MW; F88CDE1A0BEABC4F CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 SFFGAFL 279

Db 88 SFFGAFL 94

RESULT 29

Q89V44

AC Q89V44 PRELIMINARY; PRT; 220 AA.

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DE Brl1214 protein.

GN Brl1214.

OS Bradyrhizobium japonicum.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Bradyrhizobium.

OX NCBI_TaxID=375;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=USDA 110;

RE MEDLINE=22484998; PubMed=12597275;

RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,

RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,

RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,

RA Tabata S.;

RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium

RT Bradyrhizobium japonicum USDA110.";

RL DNA Res. 9:189-197(2002).

DR EMBL; AP005939; BAC46479.1; --

DR InterPro: IPR000437; Prok_LipoProt.S.

DR PROSITE; PS00013; PROK_LIPOPROTEIN; 1.

KW Complete proteome.

SQ SEQUENCE 220 AA; 23332 MW; 0AD03221F4C1A350 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 113 LVRERGE 119
Db 110 LVRERGE 116
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RESULT 30
Q8DFN8 PRELIMINARY; PRT; 222 AA.
AC Q8DFN8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Uncharacterized protein conserved in bacteria.
GN V10168.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016797; AAC08706.1; -.
KW Complete proteome.
SQ SEQUENCE 222 AA; 24807 MW; 94A0EF9F43F33FAD CRC64;

Query Match 2.5%; Score 7; DB 16; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GIFELKE 252
Db 190 GIFELKE 196
|||||

RESULT 31
P90611 PRELIMINARY; PRT; 231 AA.
ID P90611
AC P90611;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE H4 gene.
GN H4.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BK;
RX MEDLINE=20542029; PubMed=11087916;
RA Brydges S.D., Sherman G.D., Nockemann S., Loyens A., Daubener W.,
RA Dubremetz J.F., Curruthers V.B.;
RT "Molecular characterization of TgMIC5, a proteolytically processed
RT antigen secreted from the micronemes of Toxoplasma gondii.";
RL Mol. Biochem. Parasitol. 111:51-66(2000).
DR EMBL; Y09782; CAA70921.1; -.
SQ SEQUENCE 231 AA; 25984 MW; 9C5B0E4690B36314 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 FQEIKE 198
Db 137 FQEIKE 143
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RESULT 32
Q9EZK4 PRELIMINARY; PRT; 247 AA.
ID Q9EZK4
AC Q9EZK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Rot-like protein Rlp.
GN RLP.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA McNamara P.J., Milligan-Monroe K., Proctor R.A.;
RT "The Isolation and Characterization of rlp, an Activator of the
RT Staphylococcus aureus Virulence Factor Regulator Pathway Encoded by
RT agr.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288788; AAG45334.2; -.
SQ SEQUENCE 247 AA; 29792 MW; D078366866F60B2B CRC64;

Query Match 2.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 RIFVSVT 261
Db 91 RIFVSVT 97
|||||

RESULT 33
Q99RD5 PRELIMINARY; PRT; 247 AA.
ID Q99RD5
AC Q99RD5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SarH2 protein (Staphylococcal accessory regulator A homolog).
GN SARH2 OR SAV2499 OR SA2287 OR MW2418.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878; 158879, 196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP003365; BAB58661.1; -.
DR EMBL; AP003137; BAB43590.1; -.
DR EMBL; AP004830; BAB96283.1; -.
DR PIR; D90053; D90053.

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KW Complete proteome.
SQ SEQUENCE 247 AA; 29793 MW; 90AE3B0F7A87CC35 CRC64;

Query Match      2.5%; Score 7; DB 16; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 RIFVSVT 261
Db 91 RIFVSVT 97

RESULT 34
O94262
ID O94262 PRELIMINARY; PRT; 251 AA.
AC O94262;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN SPBP8B7.13.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Beck A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL032684; CAA17198.1; -.
DR PIR; T40807; T40807.
DR GeneDB SPombe; SPBP8B7.13; -.
KW Hypothetical protein.
SQ SEQUENCE 251 AA; 27746 MW; C631E344FDC0D686 CRC64;

Query Match      2.5%; Score 7; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 DPNDDES 72
Db 73 DPNDDES 79

RESULT 35
O98D64
ID O98D64 PRELIMINARY; PRT; 253 AA.
AC O98D64;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ml14839.
GN ML14839.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003005; BAB51407.1; -.
DR InterPro; IPR000160; GODEF.

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DR Pfam; PF00990; GODEF; 1.
DR SMART; SM00267; DUF1; 1.
DR TIGRPFAMs; TIGR00254; GODEF; 1.
DR PROSITE; PS00887; GODEF; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 27656 MW; 358A4F06B9866C8E CRC64;

Query Match      2.5%; Score 7; DB 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 FGAFVLVG 281
Db 168 FGAFVLVG 174

RESULT 36
Q81WU0
ID Q81WU0 PRELIMINARY; PRT; 271 AA.
AC Q81WU0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hydrolase, alpha/beta fold family.
GN BA3877.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
DR EMBL; AE017036; AAP27611.1; -.
DR TIGR; BA3877; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB hydrolase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00561; abhydrolase; 1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 271 AA; 31338 MW; D01E8F4D025FF187 CRC64;

Query Match      2.5%; Score 7; DB 16; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 RFQBEIK 197
Db 170 RFQBEIK 176

RESULT 37
Q8R0L0
ID Q8R0L0 PRELIMINARY; PRT; 293 AA.
AC Q8R0L0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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AC	Q8E313;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Hypothetical protein.
GN	GSI1776.
OS	Streptococcus agalactiae (serotype III).
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=216495;
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=NEM316 / Serotype III;
RC	MEDLINE=2242508; PubMed=12354221;
RL	Medl. Microbiol. 45:1499-1513(2002).
RL	EMBL; AL766853; CAD47435.1; -.
DR	Sagalist; gbs1776; -.
KW	Hypothenical protein; Complete proteome.
SK	SEQUENCE 298 AA; 32452 MW; 5BF7720198133368 CRC64;
Query Match	2.5%; Score 7; DB 16; Length 298;
Best Local Similarity	100.0%; Pred. No. 1.6e+02;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	24 VLLQSIC 30
Dd	92 VLLQSIC 98
RESULT 40	
Q8DXW4	
ID	Q8DXW4 PRELIMINARY; PRT; 298 AA.
AC	Q8DXW4;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Membrane protein, putative.
GN	SAGI731.
OS	Streptococcus agalactiae (serotype V).
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=216466;
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=2603 V/R / Serotype V;
RC	MEDLINE=42222988; PubMed=12200547;
RX	Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA	Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA	Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA	DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA	Radue D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA	Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarcelli M., Mora M,
RA	Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D,
RA	Rinaudo D., Rappuoli R., Telford J.L., Kaeper D.L., Grandi G.,
RA	Fraser C.M.;
RT	"Complete genome sequence and comparative genomic analysis of an
RT	emerging human pathogen, serotype V Streptococcus agalactiae.";
EL	Proc. Natl. Acad. Sci U.S.A. 99:12391-12396(2002).
DR	EMBL; AE014270; AN00594.1; -.
DR	TIGR; SAGI731; -.
KW	Complete proteome.
SK	SEQUENCE 298 AA; 32410 MW; BAF7720189133FDE CRC64;
Query Match	2.5%; Score 7; DB 16; Length 298;
Best Local Similarity	100.0%; Pred. No. 1.6e+02;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	24 VLLQSIC 30

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Db          92 VLLQSLC 98
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RESULT 41
Q96QL7      PRELIMINARY;          PRT;    318 AA.
AC Q96QL7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to cAMP responsive element binding protein-like 1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008394; AAB08394.1; -.
DR EMBL; BT007042; AAP35691.1; -.
SQ SEQUENCE 318 AA; 33894 MW; D70E20D5409C165B CRC64;

Query Match          2.5%; Score 7; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          23 TVLLQSL 29
|||||
Db          266 TVLLQSL 272
|||||

RESULT 42
Q9VI33      PRELIMINARY;          PRT;    322 AA.
AC Q9VI33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG2336 protein (AT02555p).
GN CG2336
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Rosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003674; AAF54111.1; -.
DR EMBL; AB009235; AAL89973.1; -.
DR FlyBase; FBgn0037455; CG2336.
SQ SEQUENCE 322 AA; 36891 MW; D8680A7A63BB5988 CRC64;

Query Match          2.5%; Score 7; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          207 VQIYKY 213
|||||
Db          16 VQIYKY 22
|||||

RESULT 43
Q9PEN6      PRELIMINARY;          PRT;    327 AA.
AC Q9PEN6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein XF0992.
GN XF0992
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.R., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Bonaccorsi A.A., Camargo L.E.A., Carriaro D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Frohme M., Furian L.R.,

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RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.D.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.P., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjowski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL; AF003937; AAF83802.1; --
DR PIR; H82736; H82736.
DR GO; GO:0003824; F.catalytic activity; IEA.
DR InterPro; IPR000379; Ser_estr.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 327 AA; 35553 MW; 96A5841EB1A08E90 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SPLVRER 117
Db 164 SPLVRER 170
|||||

RESULT 44
Q9ZKY9 PRELIMINARY; PRT; 329 AA.
AC Q9ZKY9
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ADP-L-glycero-D-MANNOHEPTOSE-6-epimerase.
GN GMHD OR JHP0793.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori";
RL Nature 397:176-180(1999).
DR EMBL; AF001509; AAD06369.1; --
DR PIR; D71887; D71887.
DR GO; GO:0003824; F.catalytic activity; IEA.
DR GO; GO:0009225; P.nucleotide-sugar metabolism; IEA.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 329 AA; 37351 MW; DD1003F6A8C7A720 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 RSNTLSS 138
Db 46 RSNTLSS 52
|||||

RESULT 45
Q7VJZ3 PRELIMINARY; PRT; 343 AA.
ID Q7VJZ3
AC Q7VJZ3
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE DTPD-D-glucose 4,6-dehydratase (EC 4.2.1.46).
GN HH0099.
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 51449 / 3B1;
RA Mueller S., Josenhans C., Sterzenbach T., Dreescher B., Brandt P.,
RA Bell M., Drosge M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
RT "The complete genome sequence of the carcinogenic bacterium
Helicobacter hepaticus";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
DR EMBL; AE017144; AAP76696.1; --
KW Lyase; Complete proteome.
SQ SEQUENCE 343 AA; 38920 MW; B528F6F2710A40D2 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 YIYKYTS 215
Db 329 YIYKYTS 335
|||||

RESULT 46
O84846 PRELIMINARY; PRT; 354 AA.
ID O84846
AC O84846;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein CT839.
GN CT839.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D/OW-3/CX;
RA MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis";
RL Science 282:754-759(1998).
DR EMBL; AE001356; AAC68436.1; --
DR PIR; G71465; G71465.
DR GO; GO:0016021; C.integral to membrane; IEA.
DR InterPro; IPR005495; YjgP_YjgQ.
DR Pfam; PF03739; YjgP_YjgQ; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 354 AA; 40065 MW; AD79C8F2CD59F4E5 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 354;

```
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
Db 150 KENDRIF 156

RESULT 47
Q9PL80 PRELIMINARY; PRT; 354 AA.
AC Q9PL80:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein TC0227.
GN TC0227
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / N159;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AF002289; RAF39099.1; --
DR PIR; A81728; A81728.
DR TIGR; TC0227; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005495; Yj9P_Yj9Q.
DR Pfam; PF03739; Yj9P_Yj9Q; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 354 AA; 40145 MW; E6A1317A124C10D1 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 KENDRIF 257
Db 150 KENDRIF 156

RESULT 48
Q9AVE6 PRELIMINARY; PRT; 359 AA.
AC Q9AVE6:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE OSTATC protein.
GN OSTATC OR B1080D07.14.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=21140310; PubMed=11244106;
RA Agrawal G.K., Yamazaki M., Kobayashi M., Hirochika R., Miyao A.,
RA Hirochika H.;
RT "Screening of the Rice Viviparous Mutants Generated by Endogenous
RT Retrotransposon Tos17 Insertion. Tagging of a Zeaxanthin Epoxidase
RT Gene and a Novel OSTATC Gene.";
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Plant Physiol. 125:1248-1257(2001).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
RT clone:B1080D07.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050885; BAB39766.1; --
DR EMBL; AP003203; BAB64068.1; --
DR Gramene; Q9AVE6; --
DR InterPro; IPR008277; Tat C.
DR InterPro; IPR002033; Translocase.
DR Pfam; PF00902; TatC; 1.
DR TIGRFAMs; TIGR00945; tatC; 1.
DR PROSITE; PS01218; TATC; 1.
SQ SEQUENCE 359 AA; 38763 MW; D25349B32FE1B540 CRC64;

Query Match 2.5%; Score 7; DB 10; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 DRIFVSV 260
Db 141 DRIFVSV 147

RESULT 49
Q98SU0 PRELIMINARY; PRT; 361 AA.
AC Q98SU0:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE K-Cl cotransporter (Fragment).
GN KCC.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Mount D.B., Gamba G.;
RT "Partial sequence of xKCC, a K-Cl cotransporter from Xenopus laevis.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325505; AAK28520.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000622; KCL_cotranspt1.
DR Pfam; PF03522; KCL_Cotrans_1; 1.
FT NON_TER 1
SQ SEQUENCE 361 AA; 41551 MW; 129A632D1D2EDB64 CRC64;

Query Match 2.5%; Score 7; DB 13; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 LVRRGSP 119
Db 347 LVRRGSP 353

RESULT 50
Q8WPJ2 PRELIMINARY; PRT; 367 AA.
AC Q8WPJ2:
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Endo-1,4-mannanase precursor (EC 3.2.1.78).
OS Mytilus edulis (Blue mussel).;
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OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Gill;
 RA Xu B., Janson J.C., Sellios B.;
 RT "An endo-1,4-beta-d-mannanase gene isolated from mytilus edulis.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ271365; CAC81056.1; -;
 DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0016985; F-mannan endo-1,4-beta-mannosidase activity; IEA.
 DR GO; GO:0005975; P-carbohydrate metabolism; IEA.
 KW Signal; Hydrolase; Glycosidase.
 FT SIGNAL 1 17 POTENTIAL
 FT CHAIN 18 367 ENDO-1,4-MANNANASE.
 SQ SEQUENCE 367 AA; 40956 MW; B36AE03418D2EA86 CRC64;
 Query Match 2.5%; Score 7; DB 5; Length 367;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 142 KNEKALG 148
 DB 164 KNEKALG 170
 RESULT 51
 Q7U3W6 PRELIMINARY; PRT; 374 AA.
 ID Q7U3W6
 AC Q7U3W6;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Peptide chain release factor RF-2.
 GN PRFB OR SYNW2311.
 OS Synechococcus sp. (strain WH8102).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=84588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825697; PubMed=12917641;
 RA Palenik B., Branshah B., Larimer F.W., Land M., Hauser L., Chain P.,
 RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
 RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
 RT "The genome of a motile marine Synechococcus.";
 RL Nature 424:1037-1042(2003).
 DR EMBL; BX569695; CA08826.1; -;
 KW Complete proteome.
 SQ SEQUENCE 374 AA; 41775 MW; A1FFC8C06FEB444 CRC64;
 Query Match 2.5%; Score 7; DB 16; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 93 LRTSEET 99
 DB 336 LRTSEET 342
 RESULT 52
 Q9L5E1 PRELIMINARY; PRT; 375 AA.
 ID Q9L5E1
 AC Q9L5E1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Orf, hypothetical protein (Hypothetical protein).
 GN R0207 OR HCM1.114.
 OS Salmonella typhi.
 OX Plasmid R27, and Plasmid pHCM1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R27;
 RX MEDLINE=20280091; PubMed=10773089;
 RA Sherburne C.K., Lawley T.D., Gilmour M.W., Blattner F.R., Burland V.,
 RA Grotbeck E., Rose D.J., Taylor D.E.;
 RT "The complete DNA sequence and analysis of R27, a large IncHI plasmid
 from Salmonella typhi that is temperature sensitive for transfer.";
 RL Nucleic Acids Res. 28:2177-2186(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18; PLASMID=pHCM1;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebaihia M.,
 RA Churcher C., Mungall K.L., Bentley S.D., Chillingworth T., Conerton P.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Farrar J.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar typhi C18.";
 RL Nature 413:848-852(2001).
 DR EMBL; AF250878; AAF70043.1; -;
 DR EMBL; AL513383; CAD09712.1; -;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 375 AA; 42554 MW; 9869A1E335525C0 CRC64;
 Query Match 2.5%; Score 7; DB 16; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 42 LKQMDK 48
 DB 224 LKQMDK 230
 RESULT 53
 Q8TWS8 PRELIMINARY; PRT; 375 AA.
 ID Q8TWS8
 AC Q8TWS8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Uncharacterized conserved protein.
 GN MK0954.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 and monophyly of archaeal methanogens.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 DR EMBL; AE010385; AAM02167.1; -;
 DR InterPro; IPR008934; AcPase VanPerase.
 DR InterPro; IPR002803; DUF100.
 DR Pfam; PF01950; DUF100; 1.
 DR ProDom; PD014260; DUF100; 1.
 KW Complete proteome.
 SQ SEQUENCE 375 AA; 41620 MW; 3A9F8E7BB626464C CRC64;
 Query Match 2.5%; Score 7; DB 17; Length 375;

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LRNGELV 175
Db 307 LRNGELV 313

RESULT 54
Q89SW4 PRELIMINARY; PRT; 379 AA.
AC Q89SW4;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE BLR2286 protein.
GN BLR2286.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005943; BAC47551.1; -.
KW Complete proteome.
SQ SEQUENCE 379 AA; 40061 MW; 30D67BCB25880B61 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 GPQRVAA 124
Db 170 GPQRVAA 176

RESULT 55
Q9LTH1 PRELIMINARY; PRT; 389 AA.
AC Q9LTH1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 4-nitrophenylphosphatase-like.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025605; BAA98057.1; -.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006357; HAD_SF_IIA.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMs; TIGR01460; HAD-SF-IIA; 1.

DR TIGRFAMs; TIGR01452; PGP euk; 1.
SQ SEQUENCE 389 AA; 43131 MW; 96E3D9A7BC4E0583 CRC64;

Query Match 2.5%; Score 7; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 VLLQSLC 30
Db 345 VLLQSLC 351

RESULT 56
Q9PCZ3 PRELIMINARY; PRT; 401 AA.
AC Q9PCZ3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein XF1611.
GN XF1611.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carver H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Frega J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.D., Martins E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AE003988; AAF84420.1; -.
DR PIR; C82660; C82660.
DR InterPro; IPR008928; Glyco trans fhp.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 401 AA; 46935 MW; B773581D85270510 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 DAEGYGLY 240
Db 157 DAEGYGLY 163

RESULT 57

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Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	94	RTSEETI 100							
Db	29	RTSEETI 35							
RESULT 59									
Q9UX27									
ID	Q9UX27	PRELIMINARY;	PRT;	404	AA.				
AC	Q9UX27;								
DT	01-MAY-2000	(TEMBUREl. 13, Created)							
DT	01-MAY-2000	(TEMBUREl. 13, Last sequence update)							
DT	01-JUN-2003	(TEMBUREl. 24, Last annotation update)							
DE	Amidophosphoribosyltransferase (ATASE) (Glutamine								
DE	phosphoribosylpyrophosphate amidotransferase) (GPAT) (PURF-2)								
DE	(BC 2.4.2.14)								
DE	PURF-2 OR SSO0633 OR C08 016.								
GN	Sulfolobus solfataricus.								
OS	Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;								
OC	Sulfolobus.								
OC	NCBI_TaxID=2287;								
OX	[1]								
RN	SEQUENCE FROM N.A.								
RP	STRAIN=ATCC 35092 / DSM 1617 / P2;								
RC	MEDLINE=20165948; PubMed=10701121;								
RC	Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,								
RA	Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,								
RA	Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,								
RA	Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,								
RA	St Jean A., van der Oost J., Young P., Zivanovic Y., Doolittle W.F.,								
RA	Ragan M.A., Sensen C.W.;								
RT	"Gene content and organization of the crenarchaeon Sulfolobus solfataricus P2.;"								
RT	the extremely thermophilic archaeon, Sulfolobus solfataricus P2.;"								
RL	Genome 43:1116-136(2000).								
RL	[2]								
RN	SEQUENCE FROM N.A.								
RP	STRAIN=ATCC 35092 / DSM 1617 / P2;								
RC	MEDLINE=21332296; PubMed=11427726;								
RC	She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,								
RA	Awavez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,								
RA	De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,								
RA	Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,								
RA	Thi-Ngoc H.P., Redder P., Schenk M.B., Theriault C., Tolstrup N.,								
RA	Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,								
RA	Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;								
RT	The complete genome of the crenarchaeon Sulfolobus solfataricus P2.;"								
RT	Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).								
RL	-1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE								
CC	PHOSPHORIBOSYLTRANSFERASE FAMILY.								
DR	EMBL; Y18930; CAB57667.1; -.								
DR	EMBL; AE006691; AAK40942.1; -.								
DR	PIR; G90210; G90210.								
DR	HSP; P00497; IGPH.								
DR	GO; GO:0004044; F:amidophosphoribosyltransferase activity; IEA.								
DR	GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.								
DR	GO; GO:0008152; P:metabolism; IEA.								
DR	GO; GO:0009116; P:nucleoside metabolism; IEA.								
DR	InterPro; IPR000583; GATase 2.								
DR	InterPro; IPR002375; Pr/py Ip transf.								
DR	InterPro; IPR000836; PRT:transferase.								
DR	Pfam; PF00310; GATase 2; 1.								
DR	Pfam; PF00136; Pribosyltran; 1.								
DR	PROSITE; PS00103; PUR_PYR PR TRANSFER; 1.								
KW	Glycosyltransferase; Transferase; Complete proteome.								

Db 35 YKSGIA 41

RESULT 60

Q99XN8 PRELIMINARY; PRT; 406 AA.
AC Q99XN8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative integral membrane protein.
GN LMP OR SPY2120.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
DR EMBL; AE006631; AAK34765.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar tr; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Complete proteome.
SQ SEQUENCE 406 AA; 45344 MW; 16AF61AF1E540F7E CRC64;

Query Match 2.5%; Score 7; DB 16; Length 406;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLQQLVR 89

| | | | |
Db 12 QLQQLVR 18

RESULT 61

Q9NZ26 PRELIMINARY; PRT; 406 AA.
AC Q9NZ26;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative integral membrane protein.
GN SPTM18_2178.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Bera S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).

DR EMBL; AE010119; AAL98622.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar tr; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 406 AA; 45475 MW; CC36336DD9FF8D4 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 406;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLQQLVR 89

| | | | |
Db 12 QLQQLVR 18

RESULT 62

Q8K5J7 PRELIMINARY; PRT; 406 AA.
AC Q8K5J7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative integral membrane protein.
GN LMP OR SPY13_1804 OR SPS1802.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Bera S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mamarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014171; AAM80411.1; -
DR EMBL; AP005146; BAC64897.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; sugar tr; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 45499 MW; 0824D1758512AF2B CRC64;

Query Match 2.5%; Score 7; DB 16; Length 406;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 QLRQLVR 89
 DB 12 QURQLVR 18

RESULT 63

Q8S179 PRELIMINARY; PRT; 414 AA.
 AC Q8S179;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative RNA polymerase III subunit.
 GN B1144G04.24.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
 clone:B1144G04."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003335; BAB90033.1; -.
 DR Gramene; Q8S179; -.
 DR InterPro; IPR008806; RNA_pol_Rpc82.
 DR Pfam; PF05645; RNA_pol_Rpc82; 1.
 SQ SEQUENCE 414 AA; 47142 MW; EB95244618E143DD CRC64;

Query Match 2.5%; Score 7; DB 10; Length 414;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 113 LVRERGP 119
 DB 322 LVRERGP 328

RESULT 64

Q8KIUO PRELIMINARY; PRT; 417 AA.
 AC Q8KIUO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to glycosyl transferases group 1.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22053227; PubMed=12057956;
 RA Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutayavin T.V.,
 RA Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;
 RT "Genetic Variation at the O-Antigen Biosynthetic Locus in Pseudomonas
 aeruginosa."
 RL J. Bacteriol. 184:3614-3622(2002).
 DR EMBL; AF498403; AAM27604.1; -.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR001296; Glyco trans 1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Transferase.
 SQ SEQUENCE 417 AA; 46576 MW; 2B3E3EF2B57FE76E CRC64;

Query Match 2.5%; Score 7; DB 2; Length 417;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 272 ASFFGAF 278
 DB 95 ASFFGAF 101

RESULT 65

Q8KIRO PRELIMINARY; PRT; 417 AA.
 AC Q8KIRO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to glycosyl transferases group 1.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22053227; PubMed=12057956;
 RA Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutayavin T.V.,
 RA Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;
 RT "Genetic Variation at the O-Antigen Biosynthetic Locus in Pseudomonas
 aeruginosa."
 RL J. Bacteriol. 184:3614-3622(2002).
 DR EMBL; AF498415; AAM27788.1; -.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR001296; Glyco_transf_1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Transferase.
 SQ SEQUENCE 417 AA; 46410 MW; 2265075495ABCE78 CRC64;

Query Match 2.5%; Score 7; DB 2; Length 417;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 272 ASFFGAF 278
 DB 95 ASFFGAF 101

RESULT 66

Q8I514 PRELIMINARY; PRT; 420 AA.
 AC Q8I514;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7;
 RX MEDLINE=22255705; PubMed=12368864;
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain N., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallow S.J., Su B., Peterson J., Angiuoli S.,
 RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum."
 RL Nature 419:498-511(2002).
 DR EMBL; AE014851; RAN36483.1; -.
 KW Hypothetical protein.

RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V., Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Unaway L., Tallon L.J., Gill J.E., Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;
RA	"Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.;"
RL	Nature 402:761-768 (1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Columbia;
RA	Lin X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; ACC05499; AAC67359.1; -.
DR	PIR; H84806; H84806.
DR	InterPro; IPR001810; F-box.
DR	InterPro; IPR006527; F_box_assoc.1.
DR	InterPro; IPR008945; Skp1_Skp2_.
DR	Pfam; PF00646; F-box; 1.
DR	Pfam; PF00256; FBOX; 1.
DR	SMART; SM00256; FBOX; 1.
DR	TIGRFAMs; tigr01640; F_box_assoc_1; 1.
DR	PROSITE; P50181; FBOX; 1.
SQ	SEQUENCE 424 AA; 50354 MW; 9DA14E4F834BE340 CRC64;
Query Match	
Best Local Similarity 2.5%; Score 7; DB 10; Length 424;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	56 CFLKEDD 62
Db	122 CFLKEDD 128
RESULT 69	
Q8LP64	PRELIMINARY; PRT; 425 AA.
ID	Q8LP64
AC	Q8LP64;
DT	01-OCT-2002 (T-EMBLrel. 22, Created)
DT	01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE	S-locus-related I (Fragment).
GN	SLR1.
OS	Brassica deflexa.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid1 I; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=180531;	
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=Df-1;
RC	Inaba R., Nishio T.;
RA	"Phylogenetic analysis of Brassicaceae plants based on the nucleotide sequences of S-locus related gene, SLR1.;"
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AS075409; BAB97357.1; -.
DR	GO; GO:0005529; F_sugar binding; IEA.
DR	InterPro; IPR001480; B_lectin.
DR	InterPro; IPR000858; Slocus_glycop.
DR	Pfam; PF01453; Agglutinin; 1.
DR	Pfam; PF00954; S_locus_glycop; 1.
DR	SMART; SM00108; B_lectin; 1.
FT	NON_TER 1 1
FT	NON_TER 425 425
SQ	SEQUENCE 425 AA; 48418 MW; C1ED97DAE305CF15 CRC64;
Query Match	
Best Local Similarity 2.5%; Score 7; DB 10; Length 425;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	147 LGRKINS 153

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Db      171 LGRKINS 177

RESULT 70
OB3835      PRELIMINARY;      PRT;      427 AA.
ID  O83835
AC  O83835;
DT  01-NOV-1998 (TREMBlrel. 08, Created)
DT  01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT  01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE  Nitrogen fixation protein (NIFS-2).
GN  TP0863.
OS  Treponema pallidum.
OC  Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX  NCBI_TaxID=160;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Nichols;
RX  MEDLINE=98332770; PubMed=9665876;
RA  Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA  Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA  Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA  Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA  McDonald L., Artach P., Bowman C., Cotton W.D., Fujii C., Garland S.,
RA  Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA  Venter J.C.;
RT  "Complete genome sequence of Treponema pallidum, the syphilis
RT  spirochete."
RL  Science 281:375-388(1998).
DR  EMBL; AE001256; AAC65826.1; -.
DR  FIr; G71272; G71272.
DR  TIGR; TP0863; -.
DR  GO; GO:0008483; F:transaminase activity; IEA.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro; IPR000192; AminoTrans_V.
DR  Pfam; PF00266; aminotran_5; 1.
KW  Complete proteome.
SQ  SEQUENCE 427 AA; 45732 MW; 0B5247CDBFA901AD CRC64;

Query Match      2.5%; Score 7; DB 16; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      127 TGTGRS 133
Db      166 TGTGRS 172

RESULT 71
Q9HSA2      PRELIMINARY;      PRT;      428 AA.
ID  Q9HSA2
AC  Q9HSA2;
DT  01-MAR-2001 (TREMBlrel. 16, Created)
DT  01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE  Zinc metalloproteinase homolog.
GN  CAAX OR VNG03296.
OS  Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC  Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC  Halobacteriaceae; Halobacterium.
OX  NCBI_TaxID=64091;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=20504483; PubMed=11016950;
RA  Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA  Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA  Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA  Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA  Maddocks D.G., Jablonski P.E., Krebs M.P., Argevine C.M., Dale H.,
RA  Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA  Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA  Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT  "Genome sequence of Halobacterium species NRC-1."

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RL  Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR  EMBL; AE004992; AAG18905.1; -.
DR  PIR; E84192; E84192.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR  GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR  InterPro; IPR001915; Peptidase_M48.
DR  Pfam; PF01435; Peptidase_M48; 1.
KW  Complete proteome.
SQ  SEQUENCE 428 AA; 45621 MW; 8E421F4FF1C1542D CRC64;

Query Match      2.5%; Score 7; DB 17; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      156 SSRSGHS 162
Db      237 SSRSGHS 243

RESULT 72
Q9Z913      PRELIMINARY;      PRT;      429 AA.
ID  Q9Z913
AC  Q9Z913;
DT  01-MAY-1999 (TREMBlrel. 10, Created)
DT  01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT  01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE  GMP synthase.
GN  GUA OR CPN0171 OR CP0599 OR CPB0173.
OS  Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC  Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX  NCBI_TaxID=83558;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CWL029;
RX  MEDLINE=99206606; PubMed=10192388;
RA  Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA  Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT  "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
RT  Nat. Genet. 21:385-389(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=AR39;
RX  MEDLINE=20150255; PubMed=10684935;
RA  Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA  White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
RA  Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA  Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA  Eisen J., Fraser C.M.;
RT  "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT  pneumoniae AR39."
RL  Nucleic Acids Res. 28:1397-1406(2000).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=J138;
RX  MEDLINE=20330349; PubMed=10871362;
RA  Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA  Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT  "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT  from Japan and CWL029 from USA."
RL  Nucleic Acids Res. 28:2311-2314(2000).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=TW-183;
RA  Geng M.M., Schumacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
RA  Schneider S., Pohl T., Essig A., Marte R., Melchers K.;
RT  "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT  other Chlamydia strains based on whole genome sequence analysis."
RL  Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AE001604; AAD18324.1; -.
DR  EMBL; AE002218; AAF38415.1; -.
DR  EMBL; AP002545; BAA98381.1; -.
DR  EMBL; AE017157; AAP98106.1; -.

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DR PIR; B72109; B72109.
DR PIR; C86512; C86512.
DR HSPF; P04079; 1GPM.
DR TIGR; CP0599; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0003922; F:GMP synthase (glutamine-hydrolyzing) activity; IEA.
DR GO; GO:0006177; P:GMP biosynthesis; IEA.
DR GO; GO:0006164; P:purine nucleotide biosynthesis; IEA.
DR InterPro; IPR006220; Anch_synthII.
DR InterPro; IPR000991; GATase 1.
DR InterPro; IPR001674; GMP synth C.
DR InterPro; IPR004739; GMP synth_N.
DR Pfam; PF00117; GATase; 1.
DR Pfam; PF00958; GMP synth C; 1.
DR PRINTS; PR00097; ANTSNTHASEII.
DR PRINTS; PR00096; GATASE.
DR TIGRFAMs; TIGR00888; guaA_Nterm; 1.
KW Complete proteome.
SQ SEQUENCE 429 AA; 48242 MW; DBFD3C681109BFEC CRC64;

Query Match 2.5%; Score 7; DB 15; Length 429;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 ESSRSGH 161
Db 248 ESSRSGH 254
|||||

RESULT 73
ID Q80ZJ8 PRELIMINARY; PRT; 435 AA.
AC Q80ZJ8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=olfactory epithelium;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC048916; AAH48916.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR SMART; SM00054; EPH; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 435 AA; 49006 MW; BA711CSA7DB7EB8A CRC64;

Query Match 2.5%; Score 7; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LRTSET 99
Db 147 LRTSET 153
|||||

RESULT 74
ID Q8SWZ1 PRELIMINARY; PRT; 449 AA.
AC Q8SWZ1; Q9V5Q6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RH55021p (CG12344-PA).

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GN CG12344.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Campe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jallali M., Kalush C., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster."
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,
RA Whitfield B.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
RA Lewis S.E.;
RL "Annotation of Drosophila melanogaster genome."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

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[5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AY094938; AAM11291.1; -.
DR EMBL; AE003828; AAF58743.3; -.
DR FlyBase; FBgn0033558; CG12344.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_Channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 449 AA; 51258 MW; 79EE29E409FDC648 CRC64;

Query Match 2.5%; Score 7; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 PILMKKS 225
Db |||||
442 PILMKKS 448

RESULT 75
Q7WQF5 PRELIMINARY; PRT; 457 AA.
AC Q7WQF5;
ID Q7WQF5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sensor kinase protein.
GN BB0378.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RC MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640438; CAE30876.1; -.
KW Kinase; Complete proteome.
SQ SEQUENCE 457 AA; 50053 MW; 21C76EBD1CB46265 CRC64;

Query Match 2.5%; Score 7; DB 16; Length 457;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 LLMKSAR 227
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Db |||||
233 LLMKSAR 239

Search completed: March 23, 2004, 09:23:42
Job time : 51 secs

Tue Mar 23 11:15:49 2004

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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:12:39 ; Search time 23 seconds
(without alignments)
545.440 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNLKQMDKYSKGIACFL.....NEHLMDHEASFFGAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 317993

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	72.3	177	3	US-09-105-343A-7
2	850	66.0	161	4	US-09-565-423-7
3	654	50.8	183	3	US-09-105-343A-8
4	446	34.7	85	4	US-09-632-287A-12
5	291	22.6	101	1	US-08-670-354-4
6	291	22.6	101	3	US-09-320-424-4
7	291	22.6	101	4	US-09-825-563-4
8	291	22.6	101	5	US-09-10895-4
9	245.5	19.1	87	4	US-09-632-287A-13
10	228.5	17.8	173	4	US-09-396-937-10
11	228.5	17.8	173	4	US-09-396-937-12
12	228.5	17.8	182	4	US-09-396-937-8
13	210	16.3	182	4	US-09-396-937-16
14	208	16.2	188	4	US-09-396-937-14
15	202.5	15.7	173	4	US-09-396-937-20
16	195.5	15.2	173	4	US-09-396-937-18
17	189.5	14.7	179	4	US-08-339-214-22
18	182	14.1	138	4	US-08-339-214-20
19	181.5	14.1	178	4	US-08-339-214-84
20	181.5	14.1	179	3	US-08-649-100-9
21	181.5	14.1	179	4	US-08-339-214-6
22	179	13.9	137	4	US-08-339-214-18
23	178	13.8	145	3	US-08-339-214-5
24	178	13.8	145	3	US-09-375-419-5
25	177.5	13.8	179	4	US-08-339-214-14
26	175.5	13.6	149	3	US-08-584-031-17
27	175	13.6	152	4	US-09-496-118B-8

Sequence 4, Appli
Sequence 12, Appl
Sequence 81, Appl
Sequence 5, Appl
Sequence 80, Appl
Sequence 4, Appl
Sequence 22, Appl
Sequence 79, Appl
Sequence 83, Appl
Sequence 8, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 82, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 39, Appl

138 4 US-08-339-214-4
138 4 US-08-339-214-12
138 4 US-08-339-214-81
138 4 US-09-565-423-5
139 4 US-08-339-214-80
139 4 US-08-968-686-4
141 3 US-09-286-529-22
141 3 US-08-339-214-79
141 4 US-08-339-214-83
136 4 US-08-968-686-8
137 4 US-08-339-214-2
137 4 US-08-339-214-10
137 4 US-08-339-214-82
240 3 US-08-913-014A-1
240 4 US-072-993C-4
240 4 US-09-653-285-1
174 4 US-09-131-237C-2
208 4 US-09-027-287-39

ALIGNMENTS

RESULT 1
US-09-105-343A-7
; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S. R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-105-343A-7

Query Match 72.3%; Score 930; DB 3; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.2e-88;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY

67 EKQNIPLVRGPQVAAHITGRTGRSNTLSPNSKNEKALGRKINSWESSRSHSFL 126

Db 1 EQQNISPLVERGQORVAHITGRGRNTLSPFNKNEKALGRKINSWESSRSHSFL 60
QY 127 SNLHRLNGELVHKGFGYIYISQYFRFQOEIKENTKNDKQMVQIYKYTSYDPILLMK 186
Db 61 SNLHRLNGELVHKGFGYIYISQYFRFQOEIKENTKNDKQMVQIYKYTSYDPILLMK 120
QY 187 SARNSCWSKDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 243
Db 121 SARNSCWSKDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 177

RESULT 2

US-09-565-423-7
; Sequence 7, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-7

Query Match 66.0%; Score 850; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.1e-80;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGRGRNTLSPFNKNEKALGRKINSWESSRSHSFLSNLHRLNGELVHKG 142
Db 1 RVAAHITGRGRNTLSPFNKNEKALGRKINSWESSRSHSFLSNLHRLNGELVHKG 60
QY 143 FYIYISQYFRFQOEIKENTKNDKQMVQIYKYTSYDPILLMKARNSCWSKDAEYGLY 202
Db 61 FYIYISQYFRFQOEIKENTKNDKQMVQIYKYTSYDPILLMKARNSCWSKDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 161

RESULT 3

US-09-105-343A-8
; Sequence 8, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FILE REFERENCE: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048, US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-8

Query Match 50.8%; Score 654; DB 3; Length 183;
Best Local Similarity 68.7%; Pred. No. 5.6e-60;
Matches 125; Conservative 22; Mismatches 29; Indels 6; Gaps 1;

QY 67 EQQNISPLVERGQORVAHITGRGRNTLSPFNKNEKALGRKINSWESSRSHSFL 126
Db 1 EQQNISPLVERGQORVAHITGRGRNTLSPFNKNEKALGRKINSWESSRSHSFL 60
QY 127 SNLHRLNGELVHKGFGYIYISQYFRFQOEIKENTKNDKQMVQIYKYTSYDP 180
Db 61 SNLHRLNGELVHKGFGYIYISQYFRFQOEIKENTKNDKQMVQIYKYTSYDP 120
QY 181 PILLMKARNSCWSKDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 121 PILLMKARNSCWSKDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 180
QY 241 LV 242
Db 181 II 182

RESULT 4

US-09-632-287A-12
; Sequence 12, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Pbm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-287A-12

Query Match 34.7%; Score 446; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 7.1e-39;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGQORVAHITGRGRNTLSPFNKNEKALGRKINSWESSRSHSFLSNLHRLNGELV 137

GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-4

Query Match 22.6%; Score 291; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRK 52
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDNDDESMNSPCQVKWQLRQLVRK 90

RESULT 9
US-09-632-287A-13
Sequence 13, Application US/09632287A
Patent No. 6521422
GENERAL INFORMATION:
APPLICANT: Heu, Hailing
APPLICANT: Wooden, Scott K
TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
FILE REFERENCE: 01017/35550A
CURRENT APPLICATION NUMBER: US/09/632,287A
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/147,294
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 87
TYPE: PRT
ORGANISM: Mouse

US-09-632-287A-13
Query Match 19.1%; Score 245.5; DB 4; Length 87;
Best Local Similarity 65.8%; Pred. No. 4.7e-18;
Matches 50; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

QY 81 PORVAAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHIE 140
DB 4 POKVAAHITGTRGSRNSALIPISKDKTGLQKIESWESSRKGHSFLNHLFRNGELVIEQ 63
QY 141 KGFYIYSQTYRFR 156
DB 64 E----YIYSQTYRFRQE 76

RESULT 10
US-09-396-937-10
Sequence 10, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 173
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
OTHER INFORMATION: murine OPG, residues 158-316, fused to His tag
US-09-396-937-10

Query Match 17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 7.4e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 86 AHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHIEKGFY 145
DB 22 AHLT-----INAASTPGSGHKVTL-----SSWYHDR-GWAKISNMTLSNGLRVNODGFY 71
QY 146 IYSQTYRFRQEBIKENTKNDKQVOYIVKYT--SYDPDILLMKSRNSCWSKDAEYGLYSI 204
DB 72 LVANICFRHETSGSVPTDYQLVMYVVKTSIKIPSSHNLMKGGSTKWSGSEFHFYSI 131
QY 205 YOGGIFELKENDRIFSVVTNEHLIDMDHEASFFGAFLV 242
DB 132 NVGGFFKLAGEEISIQVSNFSLDPPDQDQATYFGAFKV 169

RESULT 11
US-09-396-937-12
Sequence 12, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 22021 PC 1
CURRENT APPLICATION NUMBER: US/09/396,937
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 173

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPGn, residues 158-316 with C to S
; OTHER INFORMATION: mutation, and His tag
US-09-396-937-12

Query Match      17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred.No. 7.4e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY      86 AHITGTRGRNTLSSPNKNEKALGRKINWESSRSGHSLNHLNRNGELVIHEKGFFY 145
          ||:|||::||::||::||::||::||::||::||::||::||::||::||:
Db      22 AHLT-----INAAIPSGSHKVTL----SSWHDR-GWAKISNWTLNGLRVNQDGFY 71

QY      146 IYSQTYPFRFOEIKENTKNDQMVOYIYKYT-SYPDPILLMKSARNCSWKDAEYGLYSI 204
          :::||:::||::||::||::||::||::||::||::||::||::||::||:
Db      72 LYANISPRHHETSGSVPTDYQLMVVYVVKTSIKIPSSHNLMMKGGSTKNWSGNSEPHFYSI 131

QY      205 YQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
          ||:|||::||::||::||::||::||::||::||::||::||::||:
Db      132 NVGFFFKLRAGEEISIQVNSPLDDPDQDATYFGAFKV 169


RESULT 12
US-09-396-937-8
; Sequence 8, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC.1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR
; OTHER INFORMATION: product with optimum codons for E. coli and P.
; OTHER INFORMATION: pastoris expression
US-09-396-937-8

Query Match      17.8%; Score 228.5; DB 4; Length 187;
Best Local Similarity 34.2%; Pred.No. 8.3e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY      86 AHITGTRGRNTLSSPNKNEKALGRKINWESSRSGHSLNHLNRNGELVIHEKGFFY 145
          ||:|||::||::||::||::||::||::||::||::||::||::||:
Db      36 AHLT-----INAAIPSGSHKVTL----SSWHDR-GWAKISNWTLNGLRVNQDGFY 85

QY      146 IYSQTYPFRFOEIKENTKNDQMVOYIYKYT-SYPDPILLMKSARNCSWKDAEYGLYSI 204
          :::||:::||::||::||::||::||::||::||::||::||::||::||:
Db      86 LYANICPRHHETSGSVPTDYQLMVVYVVKTSIKIPSSHNLMMKGGSTKNWSGNSEPHFYSI 145

QY      205 YQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
          ||:|||::||::||::||::||::||::||::||::||::||::||:
Db      146 NVGFFFKLRAGEEISIQVNSPLDDPDQDATYFGAFKV 183


RESULT 13
US-09-396-937-16
; Sequence 16, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S

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QY 189 RNSCKDAEYGLYSIQGIFELKENDRIFVSTNEHLIDMDHEASFFGAFIV 242
Db 131 HLENWGNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 184

RESULT 15

US-09-396-937-20
; Sequence 20, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANNING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396.937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
; OTHER INFORMATION: P30 epitope introduced, and His tag
US-09-396-937-20

Query Match 15.7%; Score 202.5; DB 4; Length 173;
Best Local Similarity 30.2%; Pred. No. 3.7e-13;
Matches 52; Conservative 28; Mismatches 53; Indels 39; Gaps 5;
QY 86 AHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLNGLVHEKGFYY 145
Db 22 AHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKISNMTLSNGKLRVNDQGFY 71
QY 146 IYSQTYFR-----FOEIKENTKDKOMQVIYKTSYRDPILLMKARN 190
Db 72 LYANICFNFTVGFMLRVKVSASHLEVKTSLK-----IPSSHNLKGGST 117
QY 191 SCWSKDAEYGLYSIQGIFELKENDRIFVSTNEHLIDMDHEASFFGAFIV 242
Db 118 KNWGSNSEPHFYSINVGPFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 169

Search completed: March 23, 2004, 09:16:23
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:15:19 ; Search time 43 Seconds
(without alignments)

1463.399 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSGIACFL.....NEHLIDMDHBASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 644882

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	887	68.9	168	9	US-09-900-530A-10
2	878	68.2	166	9	US-09-779-050A-16
3	859	66.7	164	13	US-10-116-378-29
4	850	66.0	161	14	US-10-216-074-7
5	849	66.0	161	14	US-10-338-083-11
6	826	64.2	208	9	US-09-855-544A-16
7	746.5	58.0	188	9	US-09-855-544A-14
8	636	49.4	172	9	US-09-779-050A-17
9	446	34.7	85	14	US-10-286-696-12
10	370	28.7	113	9	US-09-855-544A-15
11	291	22.6	98	9	US-09-855-544A-10
12	278	21.6	56	15	US-10-399-018-20
13	277	21.5	88	9	US-09-855-544A-9
14	245.5	19.1	87	14	US-10-286-696-13
15	236	18.3	178	15	US-10-338-785A-2

16	233.5	18.1	199	12	US-10-289-456-86	Sequence 86, Appl
17	233.5	18.1	199	14	US-10-050-902-224	Sequence 224, App
18	233.5	18.1	199	14	US-10-050-898-224	Sequence 224, App
19	232.5	18.1	151	14	US-10-338-083-10	Sequence 10, Appl
20	232.5	18.1	158	12	US-10-289-456-101	Sequence 101, App
21	232.5	18.1	159	12	US-10-289-456-84	Sequence 84, Appl
22	232.5	18.1	160	9	US-09-779-050A-15	Sequence 15, Appl
23	232.5	18.1	165	12	US-10-289-456-103	Sequence 103, App
24	232.5	18.1	178	12	US-10-289-456-83	Sequence 83, Appl
25	232.5	18.1	180	12	US-10-289-456-100	Sequence 100, App
26	232.5	18.1	185	14	US-10-050-902-320	Sequence 320, App
27	232.5	18.1	185	14	US-10-050-898-320	Sequence 320, App
28	232.5	18.1	187	12	US-10-289-456-102	Sequence 102, App
29	230.5	17.9	170	10	US-09-791-153A-76	Sequence 76, Appl
30	230.5	17.9	193	12	US-10-289-456-96	Sequence 96, Appl
31	228.5	17.8	160	9	US-09-779-050A-14	Sequence 14, Appl
32	228.5	17.8	170	12	US-10-289-456-99	Sequence 99, Appl
33	190.5	14.8	213	14	US-10-185-425-2	Sequence 2, Appl
34	184.5	14.3	213	14	US-10-185-425-3	Sequence 3, Appl
35	177	13.8	159	14	US-10-185-425-1	Sequence 1, Appl
36	175.5	13.6	149	9	US-09-834-465-17	Sequence 17, Appl
37	175	13.6	34	14	US-10-272-411-24	Sequence 24, Appl
38	175	13.6	34	14	US-10-272-328A-24	Sequence 24, Appl
39	175	13.6	143	9	US-09-779-050A-8	Sequence 8, Appl
40	175	13.6	152	14	US-10-170-812-8	Sequence 8, Appl
41	173	13.4	138	14	US-10-216-074-5	Sequence 5, Appl
42	173	13.4	138	14	US-10-338-083-3	Sequence 3, Appl
43	173	13.4	140	13	US-10-116-378-30	Sequence 30, Appl
44	173	13.4	141	9	US-09-877-156-22	Sequence 22, Appl
45	173	13.4	143	9	US-09-779-050A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

```
US-09-900-530A-10
; Sequence 10, Application US/09900530A
; Patent No. US20020128438A1
; GENERAL INFORMATION:
; APPLICANT: Seol, Dae-Wu
; APPLICANT: Billiar, Timothy R.
; TITLE OF INVENTION: DNA Cassette for the Production of
; Secretable Recombinant Trimeric Trail Proteins, Tetracycline
; Doxycycline-Inducible Adeno-Associated Virus Vector, Their
; Doxycycline-Inducible Adeno-Associated Virus Vector, Their
; TITLE OF INVENTION: Combination and Use in Gene Therapy
; FILE REFERENCE: 5006-1-002
; CURRENT APPLICATION NUMBER: US/09/900.530A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: KR 2000-38441
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 168
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-900-530A-10
```

Query Match	68.9%	Score 887	DB 9	Length 168
Best Local Similarity	100.0%	Pred. No. 4.2e-77		
Matches 168	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	76	VREGRQVAAHITGTRGRSNTLSSPNKNEKALGRKINWESSRSGHSFLSNHLRNGE	135	
Db	1	VREGRQVAAHITGTRGRSNTLSSPNKNEKALGRKINWESSRSGHSFLSNHLRNGE	60	
QY	136	LVIHEKGFYIYSOTYFRFQBEIKENTKNDQKQVOYIYKTYSDPDPILLMKASRNSCSWK	195	
Db	61	LVIHEKGFYIYSOTYFRFQBEIKENTKNDQKQVOYIYKTYSDPDPILLMKASRNSCSWK	120	
QY	196	DAEYGLYSIOGGIFELKENDRIEFSVTNEHLIDMDHEASFGAFLVG	243	

Db 121 DAEYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168

RESULT 2

US-09-779-050A-16
; Sequence 16, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-16

Query Match 68.2%; Score 878; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.1e-76;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 78 ERGQORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 137
Db 1 ERGQORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 60
QY 138 IHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDA 197
Db 61 IHEKGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDA 120
QY 198 EYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
Db 121 EYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166

RESULT 3

US-10-116-378-29
; Sequence 29, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 29
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-29

Query Match 66.7%; Score 859; DB 13; Length 164;
Best Local Similarity 99.4%; Pred. No. 2e-74;
Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 80 GFORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 139
Db 1 GFORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 60
QY 140 EKGFFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDA 199
Db 61 EKGFFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDA 120
QY 200 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
Db 121 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 164

RESULT 4

US-10-216-074-7
; Sequence 7, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-7

Query Match 66.0%; Score 850; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 142
Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 60
QY 143 FYIYISQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDA 202
Db 61 FYIYISQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDA 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 5

US-10-338-083-11
; Sequence 11, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match      66.0%; Score 849; DB 14; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.8e-73;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 QVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 141
Db 1 QVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 60

Qy 142 GFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWSDAEYGL 201
Db 61 GFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSWSDAEYGL 120

Qy 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 242
Db 121 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 161

RESULT 6
US-09-855-544A-16
; Sequence 16, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855.544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match      64.2%; Score 826; DB 9; Length 208;
Best Local Similarity 96.3%; Pred. No. 4.1e-71;
Matches 156; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGGIACFLTKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGGIACFLTKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVREGRQVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRQVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFOEIKENT 162
Db 159 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFOEIKENT 200

RESULT 7
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855.544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-14

Query Match      58.0%; Score 746.5; DB 9; Length 188;
Best Local Similarity 61.7%; Pred. No. 1.5e-63;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

Qy 1 TNELKQMDKYSGGIACFLTKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGGIACFLTKEDDSYWDPNDESMNSPCWQVQWLRLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVREGRQVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRQVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSR 104

Qy 121 SGHSFSLNHLRNGELVTHEKGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDP 180
Db 105 -----ENTKNDKQMVQIYKYTSYDP 125

Qy 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 126 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185

Qy 241 LVG 243
Db 186 LVG 188

RESULT 8
US-09-779-050A-17
; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779.050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match      49.4%; Score 636; DB 9; Length 172;
Best Local Similarity 71.4%; Pred. No. 5.6e-53;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

Qy 81 PQVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 140
Db 4 PQVAAHITGTRGNTLTSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEK 63

Qy 141 KGFYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSW 194
Db 64 EGLYIYSQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDPILLMKSARNCSW 123

Qy 195 KDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 242
Db 124 RDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 171

RESULT 9
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailong
; APPLICANT: Wooden, Scott K
```

```
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm A No. US20030129706Alal Member of the TNF Ligand Supergene H
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-696-12

Query Match      34.7%; Score 446; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.8e-35;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGPQVAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 137
DB 1 ERGPQVAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 60

QY 138 IHBKGFYIYSQYFRPQBEIKENT 162
DB 61 IHBKGFYIYSQYFRPQBEIKENT 85

RESULT 10
US-09-855-544A-15
; Sequence 15, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo VELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-15

Query Match      28.7%; Score 370; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVRLTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVRLTSEE 98

QY 61 TISTVQEQ 69
DB 99 TISTVQEQ 107

RESULT 11
US-09-855-544A-10
; Sequence 10, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo VELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 98
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-10

Query Match      22.6%; Score 231; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVRLK 52
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQVRLK 90

RESULT 12
US-10-399-018-20
; Sequence 20, Application US/10399018
; Publication No. US20040002118A1
; GENERAL INFORMATION:
; APPLICANT: Smilansky, Zeev
; TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
; FILE REFERENCE: 9124.137USWO
; CURRENT APPLICATION NUMBER: US/10/399,018
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/IL01/00944
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: IL138946
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-018-20

Query Match      21.6%; Score 278; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 RTSEETISTVQEQKQNISPLVREGRPQVAAHITGRGRSNTLSSPNSKNEKALGR 111
DB 1 RTSEETISTVQEQKQNISPLVREGRPQVAAHITGRGRSNTLSSPNSKNEKALGR 56

RESULT 13
US-09-855-544A-9
; Sequence 9, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo VELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-9

Query Match      21.5%; Score 277; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 6.9e-19;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQQL 49
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYDNDPDEESMNSPCWQVKQLRQQL 87

RESULT 14
US-10-286-696-13
```

; Sequence 13, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. US20030129706A1 Member of the TNF Ligand Supergene F
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-10-286-696-13

Query Match 19.1%; Score 245.5; DB 14; Length 87;
Best Local Similarity 65.8%; Pred. No. 7.2e-16;
Matches 50; Conservative 9; Mismatches 14; Indels 3; Gaps 1;
QY 81 PORVAHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNLHLRNGELVHIE 140
DB 4 POKVAHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNLHLRNGELVHIE 140
QY 141 KGFYIYQTYFRFQE 156
DB 64 E--YYISQTYFRFQE 76

RESULT 15
US-10-338-785A-2
; Sequence 2, Application US/10338785A
; Publication No. US20030219864A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hubert, Rene S.
; APPLICANT: El Yazal, Jamal
; TITLE OF INVENTION: No. US20030219864A1 Variants of RANKL Protein
; FILE REFERENCE: A-71486
; CURRENT APPLICATION NUMBER: US/10/338,785A
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: construct of human RANKL extracellular region with histidine tag
; OTHER INFORMATION: and TEV protease cleavage site
US-10-338-785A-2

Query Match 18.3%; Score 236; DB 15; Length 178;
Best Local Similarity 32.7%; Pred. No. 1.6e-14;
Matches 55; Conservative 35; Mismatches 64; Indels 14; Gaps 5;
QY 79 RGPQVA---AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNLHLRNGE 135
DB 17 QGPKLEAQPAHIT-----INATDIPSGHKVSL----SSWYHDR-GWAKISNWFNSCK 66
QY 136 LVTHEKGFYIYQTYFRFQEEIKENTKNDKQMVYIYKYT-SYDPILLMKSRNSCWS 194
DB 67 LIVNQDGFYLYANICFRHHTSGDLATEYQLMWVYVTKTSIKIPSSHTLMKGGSTKYWS 126
QY 195 KDAEYGLYSYQGIGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFIV 242

DB 127 GNSEFHFYSINVGFFKLRSGEISIEVSNPSLLDPDQDQDATYFGAFKV 174
Search completed: March 23, 2004, 09:20:56
Job time : 43 secs

Db 32 KTSEETISTVQEKQONISPLVRERGPQVAAHITGTRGRSQTLSPPNSKNEKALGRKINS 91
 QY 116 WESSRSGHSLNHLRNGELVIH-BKGFYIYSQTYFRFOEIKENTKNDKQWQYIYK 174
 Db 92 WESSRSGHSLNHLRNGELVIHKEGFYIYSQTYFRFOEIKENTKNDKQWQYIYK 151
 QY 175 YTSYDPDILLMKSGARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
 Db 152 YTSYDPDILLMKSGARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 211
 QY 235 SFFGAFLVG 243
 Db 212 SFFGAFLVG 220

RESULT 2
 ID ABG72258
 XX ABG72258 standard; protein; 173 AA.
 AC
 XX
 DT 04-MAR-2003 (first entry)
 DE
 XX
 XX Partial human Trail protein, Trail109.
 XX Human; tumour related apoptosis inducing ligand; Trail109;
 XX Trail prokaryotic expression system; tumour cell death.
 XX Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 109 /note= "Encoded by CTT"
 FT
 XX
 XX CNL1354183-A.
 XX 19-JUN-2002.
 XX 30-NOV-2001; 2001CN-00132371.
 XX 30-NOV-2001; 2001CN-00132371.
 XX (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
 XX Hu Y, Yao Y;
 XX WPI; 2002-751439/82.
 XX N-PSDB; ABX14392.
 XX Tumor death induction ligand gene, gene expression protein and its
 XX preparation method.
 XX Claim 7; Page 10 (disclosure); 17pp; Chinese.
 XX The present invention relates to the isolation of cDNA encoding human
 XX tumour related apoptosis inducing ligand (Trail), and the Trail protein.
 XX The Trail full length cDNA is cloned, and is utilised to create a Trail
 XX prokaryotic expression system. The full length Trail cDNA is used to
 XX respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
 XX 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
 XX expression systems. The prokaryotic expression systems created greatly
 XX increase the expression and quantity of the Trail, Trail109, and Trail114
 XX proteins, and may be useful in a new preparation for killing tumour
 XX cells. The present sequence represents the partial human Trail protein,
 XX Trail109
 XX Sequence 173 AA;
 XX Query Match 70.5%; Score 907; DB 5; Length 173;
 XX Best Local Similarity 99.4%; Pred. No. 1.9e-80;
 XX Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 71 NISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHL 130

Db 1 NISPLVRERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHL 60
 QY 131 LRNGELVIHKEGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSGAR 190
 Db 61 LRNGELVIHKEGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSGAR 120
 QY 191 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
 Db 121 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 173

RESULT 3
 ABB76826
 ID ABB76826 standard; protein; 168 AA.
 XX
 AC ABB76826;
 XX
 DT 16-JUL-2002 (first entry)
 DE
 XX
 XX Human TRAIL.
 XX Human; TRAIL; tumour necrosis factor; TNF;
 XX tumour necrosis factor related apoptosis inducing ligand; TRAIL; cancer;
 XX viral infection; cytostatic.
 XX Homo sapiens.
 XX OS
 XX KR2001019100-A.
 XX PD 15-MAR-2001.
 XX PF 25-AUG-1999; 99KR-00035354.
 XX PR 25-AUG-1999; 99KR-00035354.
 XX (DONG-) DONG WHA PHARM IND CO LTD.
 XX Cha SS, Kim JU, Lee GJ, Lim GM, Oh BH, Yoon JI, Yoon SJ;
 XX WPI; 2001-533833/59.
 XX N-PSDB; ABL53366.
 XX
 PT Producing and crystallizing tumor necrosis factor related apoptosis
 PT inducing ligand protein, and its three-dimensional structure.
 XX Claim 1; Page 14; 20pp; Korean.
 XX The present invention relates to a method for producing Tumour Necrosis
 XX Factor (TNF) related Apoptosis inducing ligand (TRAIL) protein, and for
 XX crystallising the TRAIL protein and its three-dimensional structure,
 XX where the TRAIL protein has improved activity, which specifically kills
 XX cancer cells and cells infected by virus. The present sequence is human
 XX TRAIL, which was used in the invention
 XX Sequence 168 AA;
 XX Query Match 68.9%; Score 887; DB 4; Length 168;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e-78;
 XX Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 76 VREERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 135
 Db 1 VREERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 60
 QY 136 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSGARNSCK 195
 Db 61 LVTHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYDPDILLMKSGARNSCK 120
 QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
 Db 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 4
AAU99896
XX AAU99896 standard; protein; 168 AA.
AC AAU99896;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human TNF related apoptosis including ligand (TRAIL) protein.
XX
XX TRAIL; TNF receptor apoptosis including ligand; human; SDR5;
XX
XX tumour necrosis factor; crystal structure; TRAIL-SDR5 complex; apoptosis.
XX
XX Homo sapiens.
XX
XX W0200253727-A1.
XX
XX 11-JUL-2002.
XX
XX 10-JAN-2001; 2001WO-KR000034.
XX
XX 29-DEC-2000; 2000KR-00085947.
XX
XX (DONG-) DONG WHA PHARM IND CO LTD.
XX
XX (UYPO-) UNIV FOHANG SCI & TECHNOLOGY.
XX
XX Chung YH, Ryu JM, Hwang YH, Yoon JI, Lim KM, Oh B, Cha S;
XX
XX WPI; 2002-583613/62.
XX
XX Novel expression vector containing an sDR5 encoding gene transformed into
XX
XX Escherichia coli to produce sDR5 protein for crystallizing a tumor
XX
XX necrosis factor-related apoptosis-inducing ligand-sDR5 complex.
XX
XX Claim 5; Page 70; 74pp; English.
XX
XX This invention relates to an expression vector containing the tumour
XX
XX necrosis factor related apoptosis inducing ligand (TRAIL) protein
XX
XX receptor SDR5. The invention also comprises a method for producing the
XX
XX SDR5 protein from an E. coli transformed with the vector. The method of
XX
XX the invention is useful for crystallising the TRAIL-SDR5 complex. A TRAIL
XX
XX -SDR5 crystal complex is useful for developing recombinant proteins i.e.
XX
XX proteins with improved stability or cytotoxic activity of a TRAIL protein
XX
XX which involves changing the amino acid of the AA loop to increase the
XX
XX various interactions between amino acids or from the binding site of
XX
XX metal ions or the disulfide bonding, or changing the corresponding amino
XX
XX acids of the homotrimer interface or homodimer interface to increase the
XX
XX various interactions between amino acids or from the binding site of
XX
XX metal ion or disulfide bond, or to fill the cavity. A 3 dimensional
XX
XX structure of the TRAIL-SDR5 complex is useful for the molecular strategy
XX
XX conferring specificity for the recognition between TNF family members and
XX
XX TNF receptor family members and for the development of TRAIL protein,
XX
XX which has a better stable, cytotoxic activity or an improved receptor
XX
XX binding affinity. The present sequence represents the human tumour
XX
XX necrosis factor receptor apoptosis inducing ligand (TRAIL) protein
XX
XX sequence used in the invention
XX
XX Sequence 168 AA;
XX
XX Query Match 68.9%; Score 887; DB 5; Length 168;
XX
XX Best Local Similarity 100.0%; Pred. NO. 1.6e-78;
XX
XX Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 76 VREGRQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 135
XX
XX 1 VREGRQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 60
XX
XX 136 LVTHKEGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSK 195
XX
XX 61 LVTHKEGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSK 120
XX
XX 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
XX
XX Query Match 68.5%; Score 882; DB 5; Length 168;
XX
XX Best Local Similarity 99.4%; Pred. NO. 5.1e-78;
XX
XX Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 76 VREGRQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 135
XX
XX 1 VREGRQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 60
XX
XX 136 LVTHKEGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSK 195
XX
XX 61 LVTHKEGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSK 120
XX
XX 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
XX
XX 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168

Db 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168

RESULT 5
ABG72259
ID ABG72259 standard; protein; 168 AA.
XX
XX ABG72259;
XX
XX 04-MAR-2003 (first entry)
XX
XX Partial human Trail protein, Trail114.
XX
XX Human; tumour related apoptosis inducing ligand; Trail114;
XX
XX Trail prokaryotic expression system; tumour cell death.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 104 /note= "Encoded by CTT"
XX
XX CN1354183-A.
XX
XX 19-JUN-2002.
XX
XX 30-NOV-2001; 2001CN-00132371.
XX
XX 30-NOV-2001; 2001CN-00132371.
XX
XX (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
XX
XX Hu Y, Yao Y;
XX
XX WPI; 2002-751439/82.
XX
XX N-PSDB; ABX14393.
XX
XX Tumour death induction ligand gene, gene expression protein and its
XX
XX preparation method.
XX
XX Claim 7; Page 10 (disclosure); 17pp; Chinese.
XX
XX The present invention relates to the isolation of cDNA encoding human
XX
XX tumour related apoptosis inducing ligand (Trail), and the Trail protein.
XX
XX The Trail full length cDNA is cloned, and is utilised to create a Trail
XX
XX prokaryotic expression system. The full length Trail cDNA is used to
XX
XX respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
XX
XX 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
XX
XX expression systems. The prokaryotic expression systems created greatly
XX
XX increase the expression and quantity of the Trail, Trail109, and Trail114
XX
XX proteins, and may be useful in a new preparation for killing tumour
XX
XX cells. The present sequence represents the partial human Trail protein,
XX
XX Trail114
XX
XX Sequence 168 AA;
XX
XX Query Match 68.5%; Score 882; DB 5; Length 168;
XX
XX Best Local Similarity 99.4%; Pred. NO. 5.1e-78;
XX
XX Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 76 VREGRQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 135
XX
XX 1 VREGRQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 60
XX
XX 136 LVTHKEGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSK 195
XX
XX 61 LVTHKEGFYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDILLMKSRNSCWSK 120
XX
XX 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
XX
XX 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168


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XX AC ABR84402;
XX DT 09-OCT-2003 (first entry)
XX DE TRAIL amino acid sequence.
XX KW TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosis.
XX OS Unidentified.
XX PN CN1380339-A.
XX PD 20-NOV-2002.
XX PF 10-APR-2001; 2001CN-00105946.
XX PR 10-APR-2001; 2001CN-00105946.
XX PA (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
XX PI Li B, Gao X, Liu Z;
XX DR WPI; 2003-230973/23.
XX DR N-PSDB; ACC83357.
XX PT Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for
XX PT inducing the death of tumor cells, is related to mutational human tumor
XX PT necrosis.
XX PS Claim 4; Fig 2; 14pp; Chinese.
XX CC The invention relates to a TNF-related apoptosis-inducing ligand encoding
XX CC (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is
XX CC related to mutational human tumor necrosis. The polypeptide of the
XX CC invention is useful for inducing the death of tumor cells. The current
XX CC sequence represents the TRAIL amino acid sequence
XX SQ Sequence 167 AA;

Query Match 67.3%; Score 866; DB 6; Length 167;
Best Local Similarity 98.2%; Pred. No. 1.9e-76;
Matches 166; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 75 LVREGRQVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNG 134
DB 1 MVRERG-RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNG 58
QY 135 ELVIHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 194
DB 59 ELVIHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 118
QY 195 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
DB 119 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 167

RESULT 8
AAY71985
ID AAY71985 standard; protein; 161 AA.
XX AC AAY71985;
XX DT 28-MAR-2001 (first entry)
XX DE C-terminal region of human TRAIL protein.
XX KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
XX KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;

Query Match 68.2%; Score 878; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e-77;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGPQVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 137
DB 1 ERGPQVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 60
QY 138 IHEKGFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWSKDA 197
DB 61 IHEKGFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWSKDA 120
QY 198 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
DB 121 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166

RESULT 7
ABR84402
ID ABR84402 standard; protein; 167 AA.

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```

XX AC ABR84402;
XX DT 09-OCT-2003 (first entry)
XX DE TRAIL amino acid sequence.
XX KW TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosis.
XX OS Unidentified.
XX PN CN1380339-A.
XX PD 20-NOV-2002.
XX PF 10-APR-2001; 2001CN-00105946.
XX PR 10-APR-2001; 2001CN-00105946.
XX PA (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
XX PI Li B, Gao X, Liu Z;
XX DR WPI; 2003-230973/23.
XX DR N-PSDB; ACC83357.
XX PT Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for
XX PT inducing the death of tumor cells, is related to mutational human tumor
XX PT necrosis.
XX PS Claim 4; Fig 2; 14pp; Chinese.
XX CC The invention relates to a TNF-related apoptosis-inducing ligand encoding
XX CC (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is
XX CC related to mutational human tumor necrosis. The polypeptide of the
XX CC invention is useful for inducing the death of tumor cells. The current
XX CC sequence represents the TRAIL amino acid sequence
XX SQ Sequence 167 AA;

Query Match 67.3%; Score 866; DB 6; Length 167;
Best Local Similarity 98.2%; Pred. No. 1.9e-76;
Matches 166; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 75 LVREGRQVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNG 134
DB 1 MVRERG-RVAAHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLSNLHRLNG 58
QY 135 ELVIHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 194
DB 59 ELVIHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYDPDILLMKSARNCSWS 118
QY 195 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
DB 119 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 167

RESULT 8
AAY71985
ID AAY71985 standard; protein; 161 AA.
XX AC AAY71985;
XX DT 28-MAR-2001 (first entry)
XX DE C-terminal region of human TRAIL protein.
XX KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
XX KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;

```

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 2..8
 FT /label= Beta_strand.
 FT Region 32..34
 FT /label= Beta_strand
 FT Region 42..44
 FT /label= Beta_strand
 FT Region 47..50
 FT /label= Beta_strand
 FT Region 53..56
 FT /label= Beta_strand
 FT Region 61..72
 FT /label= Beta_strand
 FT Region 86..91
 FT /label= Beta_strand
 FT Region 99..109
 FT /label= Beta_strand
 FT Region 118..128
 FT /label= Beta_strand
 FT Region 133..143
 FT /label= Beta_strand
 FT Region 153..160
 FT /label= Beta_strand

XX WO200068378-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US012266.

XX 06-MAY-1999; 99US-0132892P.

XX 01-MAY-2000; 2000US-0201012P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI; 2001-016094/02.

XX Isolated TALL-1 protein is used to identify compounds that regulate B
 FT lymphocyte proliferation, used to treat B lymphocyte associated
 FT autoimmune disorders.

XX Example 1; Fig 1b; 112pp; English.

XX The present invention relates to Tumour necrosis factor (TNF) and Apol-
 CC related leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
 CC proteins (including homologues), and their antibodies. The invention in
 CC particular relates to methods for regulating the interaction between TALL
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
 CC TALL-1 protein is useful for identifying compounds that regulate B
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte
 CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a C-terminal region of human TRAIL protein, which
 CC has 20-25% sequence identity with the C-terminal region of human TALL-1
 CC protein extracellular domain. TRAIL protein is a TNF family member

XX Sequence 161 AA;

Query Match 66.0%; Score 850; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 6.5e-75;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVITHEKG 142

Db 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVITHEKG 60

Oy 143 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAARNSCWSKDAEYGLY 202

Db 61 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSAARNSCWSKDAEYGLY 120

Oy 203 SIYQGGIFELKENDRIEFSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 SIYQGGIFELKENDRIEFSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 9

ABR39855

ID ABR39855 standard; protein; 161 AA.

XX ABR39855;

AC 11-AUG-2003 (first entry)

DT TNF family member, TRAIL (1d4v) protein fragment.

DE RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;

XX RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;

XX tumour necrosis factor; TNF; TRAIL; cytokine.

XX Unidentified.

XX WO2003014077-A2.

XX 20-FEB-2003.

XX 09-AUG-2002; 2002WO-US025287.

XX 09-AUG-2001; 2001US-0311163P.

XX 22-MAR-2002; 2002US-00105057.

XX (BARN-) BARNES-JEWISH HOSPITAL.

XX Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;

XX WPI; 2003-256526/25.

XX Composition for identifying a compound with Receptor Activator of
 FT Necrosis Factor kB, RANK modulating activity and for identifying RANK or
 FT osteoprotegerin modulating compound, has a protein complex in crystalline
 FT form.

XX Disclosure; Fig 3; 66pp; English.

XX The invention relates to a composition (I) comprising a protein complex
 CC in crystalline form, where the complex comprises an amino acid sequence
 CC of a Receptor Activator of Necrosis Factor kB (RANK) Ligand (RANKL)
 CC ectodomain. (I) is useful for identifying a compound with RANK modulating
 CC activity, and for identifying a RANK or RANK modulating compound. (I) is
 CC useful to intelligently design mutants that have altered biological
 CC properties and for identifying and/or designing compounds that bind RANK
 CC as an approach towards developing new therapeutic agents. (I) is also
 CC useful to computationally screen small molecule databases for chemical
 CC entities or compounds that can bind in whole, or in part, to RANK or
 CC RANKL. The present sequence represents a tumour necrosis factor (TNF)
 CC family member, TRAIL (1d4v), used in a structural-based alignment study
 CC of murine RANKL protein

XX Sequence 161 AA;

Query Match 66.0%; Score 850; DB 6; Length 161;
 Best Local Similarity 100.0%; Pred. No. 6.5e-75;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVITHEKG 142

Db 1 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVHIEKG 60
 QY 143 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 202
 Db 61 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 120
 QY 203 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
 Db 121 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 10
 ADC03335
 ID ADC03335 standard; protein; 161 AA.
 XX AC ADC03335;
 XX DT 18-DEC-2003 (first entry)
 XX DE Tumour necrosis factor family cytokine, TRAIL.
 XX KW RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPG;
 KW bone-forming compound; tumour necrosis factor; TNF family; cytokine;
 KW TRAIL.
 XX OS Mus sp.
 XX PN US2003050223-A1.
 XX PD 13-MAR-2003.
 XX PF 09-AUG-2002; 2002US-00215446.
 XX PR 09-AUG-2001; 2001US-0311163P.
 XX PA (LAMJ/) LAM J.
 PA (ROSS/) ROSS F P.
 PA (TEIT/) TEITELBAUM S L.
 PA (NELS/) NELSON C A.
 PA (FREM/) FREMONT D H.
 XX PI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
 XX WPI; 2003-605763/57.
 XX Composition comprising crystalline receptor activator of NFkappaB (RANK)
 PT ligand ectodomain complex whose three-dimensional structural
 PT representation is useful for identifying RANK or osteoprotegerin
 PT modulating compound.
 XX PS Disclosure; Fig 3; 40pp; English.

The invention relates to a composition comprising a protein complex in
 CC crystalline form, where the complex comprises an amino acid sequence of a
 CC receptor activator of nuclear factor kappaB (NFkappaB) (RANK) ligand
 CC (RANKL) ectodomain. The three-dimensional structural representation of a
 CC RANKL ectodomain crystal complex, is useful for identifying a RANK or
 CC osteoprotegerin (OPG) modulating compound, and for identifying a compound
 CC with RANK modulating activity. The crystals permit the determination of
 CC the three-dimensional X-ray diffraction structure of the crystal-line
 CC polypeptide to high resolution. The atomic structure coordinates and
 CC structural information which comprises atomic structure coordinates and
 CC useful for identifying bone-forming compounds by methods which utilise
 CC the coordinates for solving the three-dimensional X-ray diffraction
 CC and/or solution structures of other proteins, including mutant forms, to
 CC high resolution. The structural information may also be used in a variety
 CC of molecular modeling and computer-based screening applications to, for
 CC example design mutants of the crystallized RANKL, its receptors, or a
 CC portion or fragment of RANKL or its receptors. The coordinates of RANKL
 CC crystal, or subsets of such structural coordinates of the RANKL crystal,
 CC are useful for designing or identifying candidate compounds capable of
 CC modulating RANK biological activity, and for identifying compounds which

CC mimic the capability of RANKL to bind RANK molecules, thereby activating
 CC the receptor. The present sequence represents the amino acid sequence of
 CC the tumour necrosis factor family cytokine, TRAIL.
 XX Sequence 161 AA;
 QY Query Match 66.0%; Score 850; DB 7; Length 161;
 CC Best Local Similarity 100.0%; Pred. No. 6.5e-75;
 XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 83 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVHIEKG 142
 Db 1 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSPFLSNHLRNGELVHIEKG 60
 QY 143 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 202
 Db 61 FYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 120
 QY 203 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
 Db 121 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 161

RESULT 11
 AAU99301
 ID AAU99301 standard; protein; 212 AA.
 XX AC AAU99301;
 XX DT 24-SEP-2002 (first entry)
 XX DE Human TRAIL splice variant 8, rpl-6-6, protein.
 XX KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
 KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
 KW TRAIL; apoptosis; programmed cell death; differentiation; development;
 KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
 KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
 KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
 KW chromosome 3q26; rpl-6-6.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Domain 1..16 /note= "Cytoplasmic domain"
 FT Domain 17..38 /note= "Transmembrane domain"
 FT Domain 39..212 /note= "Extracellular domain"
 FT Misc-difference 209 /note= "Encoded by in-frame stop codon"
 XX PN US2002061525-A1.
 XX PD 23-MAY-2002.
 XX PF 16-MAY-2001; 2001US-00855544.
 XX PR 16-MAY-2000; 2000IL-00136156.
 XX PA (YELI/) YELIN R.
 PA (KHOS/) KHOSRAVI R.
 PA (SAVI/) SAVITZKY K.
 XX PI Yelin R, Khosravi R, Savitzky K;
 XX WPI; 2002-479259/51.
 XX New splice variants of tumor necrosis factor-related apoptosis inducing
 PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
 PT diseases or disorders associated with low expression of the variants.
 XX

Claim 4; Fig 8; 29pp; English.

The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumor necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the induction of apoptosis of tumour cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the human TNF-related apoptosis inducing ligand (TRAIL) splice variant 8, rpi-6-6, protein which has had an C-terminal section of the conserved TNF domain deleted

Sequence 212 AA;

Query Match 64.3%; Score 827; DB 5; Length 212;
Best Local Similarity 91.3%; Pred. No. 1.7e-72;
Matches 159; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGTACFLKEDDSYWDNDPDESNMSPCWQVKQRLVLRKMLRTSEE 60
DB 39 TNELKQMDKYKSGTACFLKEDDSYWDNDPDESNMSPCWQVKQRLVLRKMLRTSEE 98
QY 61 TISTVQEKQNI SPLVRERGPQVAHI TGTGRKSNLTSPNKGKALGRKINSWESSR 120
DB 99 TISTVQEKQNI SPLVRERGPQVAHI TGTGRKSNLTSPNKGKALGRKINSWESSR 158
QY 121 SGHSFSLNLRNGELVIHKGFIYYSQYFRFQBEIKENTKNDKQMVQYIY 173
DB 159 SGHSFSLNLRNGELVIHKGFIYYSQYFRFQBEIKENTKNDKQMVQYIY 211

RESULT 12

AAU79599

ID AAU79599 standard; protein; 188 AA.

XX AAU79599;

AC AAU79599;

DT 24-SEP-2002 (first entry)

DE Human TRAIL splice variant 6, TRA-33-T7, protein.

XX Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
XX tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26; TRA-33-T7.

Homo sapiens.

OS Key Location/Qualifiers
XX FH Domain 1..16 "Cytoplasmic domain"
FT Domain 17..38
FT Domain /note= "Transmembrane domain"
FT Domain 39..188
FT Domain /note= "Extracellular domain"

XX US2002061525-A1.

XX 23-MAY-2002.

XX 16-MAY-2001; 2001US-00855544.

XX 16-MAY-2000; 2000IL-00136156.

XX (YELI/) YELIN R.

XX (KHOS/) KHOSRAVI R.

XX (SAVI/) SAVITZKY K.

XX Yelin R, Khosravi R, Savitzky K;

XX WPI; 2002-479259/51.

XX New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.

Claim 4; Fig 9; 29pp; English.

The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumor necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms. Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity. Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the human TNF-related apoptosis inducing ligand (TRAIL) splice variant 6, TRA-33-T7, protein which has had an N-terminal section of the conserved TNF domain deleted

Sequence 188 AA;

Query Match 58.0%; Score 746.5; DB 5; Length 188;

Best Local Similarity 61.7%; Pred. No. 1.1e-64;

Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDNDPDESNMSPCWQVKQRLVLRKMLRTSEE 60

Db 39 TNELKQWQDYKSGIACFLKEDDSYWDPNDESSMSPCWQVKQLRQKMLRTSEE 98
Qy 61 TISTVQEQQNI SPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 120
Db 99 TISTVQ-----104
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYT 180
Db 105 -----ENTKNDKQMVQYIYKYT 125
Qy 181 PILLMKARSNSKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 126 PILLMKARSNSKDAEYGLYSIQGGIPELKENDRIFVSVTNEHLIDMDHEASFFGAF 185
Qy 241 LVG 243
Db 186 LVG 188
RESULT 13
ID AAY01518
XX AAY01518 standard; peptide; 139 AA.
AC AAY01518;
XX
XX 27-MAY-1999 (first entry)
DT
DE Polypeptide of the invention.
XX
XX Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX
XX Homo sapiens.
OS
XX
XX FR2766713-A1.
PN
XX
XX 05-FEB-1999.
PD
XX
XX 04-AUG-1997; 97FR-00010176.
PF
XX
XX 04-AUG-1997; 97FR-00010176.
PR
XX
XX (INMR) BIO MERIEUX.
PA
XX
XX Rieger F, Belliveau JF, Perron H;
PI
XX
XX WPI; 1999-156177/14.
DR
XX
XX Use of polypeptide derived from TRAIL protein for diagnosis of
PT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.
XX
XX
XX Claim 5; Page 14; 21pp; French.
PS
XX
XX The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part AAY01516-17 to produce a diagnostic,
CC prophylactic or therapeutic composition useful in cases of degenerative,
CC autoimmune and inflammatory diseases. The polypeptides can be used in
CC treatment of neurodegenerative diseases, lupus erythematosus, rheumatoid
CC arthritis, and SEP. The polypeptides are apoptotic in central nervous
CC system cells, antigenic and specifically recognise the surface receptor
CC of the TRAIL protein. The polypeptide is a marker of disease and a
CC therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex. The present sequence
CC represents a polypeptide of the invention
XX
XX Sequence 139 AA;
SQ
Query Match 56.5%; Score 727; DB 2; Length 139;

Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 57 TSEETISTVQEQQNI SPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 116
Db 1 TSEETISTVQEQQNI SPLVRRGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 60
Qy 117 ESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYT 176
Db 61 ESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEEIKENTKNDKQMVQYIYKYT 120
Qy 177 SYDPDPILLMKARSNSK 195
Db 121 SYDPDPILLMKARSNSK 139
RESULT 14
ID AAB08275
XX AAB08275 standard; protein; 172 AA.
AC AAB08275;
XX
XX 04-DEC-2000 (first entry)
DT
DE Amino acid sequence of a mouse TNF ligand TRAIL.
XX
XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.
XX
XX Mus sp.
OS
XX
XX WO200047740-A2.
PN
XX
XX 17-AUG-2000.
PD
XX
XX 11-FEB-2000; 2000WO-US003653.
PF
XX
XX 12-FEB-1999; 99US-0119906P.
PR
XX
XX 18-NOV-1999; 99US-0166271P.
PR
XX
XX (AMGB-) AMGEN INC.
PA
XX
XX Boyle WJ, Hsu H;
PI
XX
XX WPI; 2000-558217/51.
DR
XX
XX Novel polypeptides comprising tumor necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis.
PT
XX
XX Claim 14; Fig 9; 71pp; English.
PS
XX
XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand family
CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell
CC stimulatory factor. Expression of AGP-3 correlates to increases in the
CC number of B cells and immunoglobulins produced. AGP-3 proteins,
CC antibodies, and nucleic acids may be used to treat inflammatory and
CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
CC graft versus host disease. The nucleic acids may be used to regulate the
CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
CC and nucleic acids are also useful for the detection of AGP-3 agonists,
CC antagonists and characterizing interactions with AGP-3 related proteins
XX
XX SQ Sequence 172 AA;
Query Match 49.2%; Score 633; DB 3; Length 172;
Best Local Similarity 71.4%; Pred. No. 1.3e-53;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;
Qy 81 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHE 140

```
Db 4 POKVAAHITGTRRNSALIPISKDGTKLGQKIESWESSRKGHSFLNHLVPRNGELVIEQ 63
QY 141 KGFVYYSQYFFFOEB-----IKENTKNDKQWQYIYKYTSYPPDPILLMKSGARNSCWS 194
Db 64 EGYLYYSQYFFFOEAEADASKVSKVKRTKQLVQYIYKYTSYPPDFIVLMKSGARNSCWS 123
QY 195 KDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHEASFFGAFV 242
Db 124 RDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDLQEAFFGAFV 171

RESULT 15
AAG03752
ID AAG03752 standard; protein; 121 AA.
XX AC AAG03752;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein, SEQ ID NO: 7833.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-00200610.
XX PR 26-FEB-1999; 99US-0122487P.
XX PA (GEST ) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX DR WPI; 2000-500381/45.
XX DR N-PSDB; AAC03758.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 13; SEQ ID NO 7833; 71pp + Sequence Listing; English.
XX CC The present sequence is a polypeptide encoded by one of a large number of
XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated
XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT
XX CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX CC sequences derived from the 5' ends of mRNAs and even in those cases where
XX CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX CC are also used in diagnostic, forensic, gene therapy and chromosome
XX CC mapping procedures. They are used to obtain upstream regulatory sequences
XX CC and to design expression and secretion vectors
XX SQ Sequence 121 AA;

Query Match 33.0%; Score 425; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDPNDESMNSPCWQVKWQLRQVLRKMLRTSEE 60
Db 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESMNSFCWQVKWQLRQVLRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVREG 80
```

```
Db 99 TISTVQEKQONISPLVREG 118

Search completed: March 23, 2004, 09:13:49
Job time : 62 secs
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:11:39 ; Search time 20 Seconds
(without alignments)
1168.727 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYSKSIACFL.....NEHLIDMDHPSFGAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 125680

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: Piri: *
2: Piri2: *
3: Piri3: *
4: Piri4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134.5	10.5	204	1 S17289	tumor necrosis fac
2	131.5	10.2	234	1 A25451	tumor necrosis fac
3	130	10.1	232	1 S12606	tumor necrosis fac
4	129.5	10.1	235	2 I54490	tumor necrosis fac
5	127.5	9.9	204	1 S24641	lymphotoxin - bovi
6	126	9.8	234	1 JQ1344	tumor necrosis fac
7	123	9.6	233	1 QWHUN	tumor necrosis fac
8	122	9.5	205	1 QWHUX	lymphotoxin alpha
9	121	9.4	235	1 QWMSN	tumor necrosis fac
10	121	9.4	235	2 JU0029	tumor necrosis fac
11	120	9.3	233	1 S22052	tumor necrosis fac
12	117.5	9.1	234	1 JH0529	tumor necrosis fac
13	115.5	9.0	193	2 S06192	tumor necrosis fac
14	114	8.9	202	1 S27303	tumor necrosis fac
15	113.5	8.8	185	2 S22715	tumor necrosis fac
16	113	8.8	233	1 S24642	tumor necrosis fac
17	111.5	8.7	202	1 JN0869	tumor necrosis fac
18	107	8.3	197	1 JH0309	tumor necrosis fac
19	98.5	7.7	233	2 S11688	tumor necrosis fac
20	80.5	6.3	203	2 C89803	hypothetical prote
21	78	6.1	202	2 A82076	conserved hypotet
22	77	6.0	223	2 H71485	hypothetical prote
23	76.5	5.9	195	2 S77753	peptide transport
24	75.5	5.9	142	2 B87569	dnak suppressor pr
25	74	5.7	201	2 E82910	hypothetical prote
26	73	5.7	223	2 B64396	hypothetical prote
27	73	5.7	227	2 E70438	hypothetical prote
28	72.5	5.6	112	2 AF0347	conserved hypotet
29	72.5	5.6	123	2 T26862	hypothetical prote

ALIGNMENTS

RESULT 1

S17289

tumor necrosis factor beta precursor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: S17289

R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative an

A;Reference number: S17289; MUID:91340150; PMID:1874444

A;Accession: S17289

A;Molecule type: DNA

A;Residues: 1-204 <KUH>

A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133

A;Genetics: 32/3; 68/1

A;Introns: 32/3; 68/1

C;Superfamily: tumor necrosis factor

C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

F;1-33/Domain: signal sequence #status predicted <SIG>

F;34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match 10.5%; Score 134.5; DB 1; Length 204;

Best Local Similarity 24.7%; Pred. No. 0.00037;

Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

QY 63 STVQEKQNMISPLVRERGQORVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS 115

Db 42 SAAQPAHQH-PPKHLAGTLKPAHLVGDPTDPSLRWRANT-----DRAFLR---- 88

QY 116 WESSRSGHSLNHLRNGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY 175

Db 89 -----HGFL-----LSNNSLLVPTSLGYFVYSQVVSFGEGCFPKATPTPLYLAHEVQLP 137

QY 176 TS-YPPPIILLMKARSCHSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 234

Db 138 SSOYFPHVLLSAQKSCVCPQGPW-VRSVYQGAFLLTQGDQLSTHTDGTPLLHSPSS 196

QY 235 SFFGAF 240

Db 197 VFFGAF 202

RESULT 2

A25451

tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C;Accession: A25451; J50727

R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H

DNA 5, 149-156, 1986

A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for ra

A;Reference number: A25454; MUID:86219711; PMID:3519137
 A;Accession: A25454
 A;Molecule type: mRNA
 A;Residues: 1-234 <ITO>
 A;Cross-references: GB:W12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A;Reference number: A25451; MUID:86219712; PMID:3519138
 A;Accession: A25451
 A;Molecule type: DNA
 A;Residues: 1-234 <IT2>
 A;Note: this sequence differs from that shown in having a Gln inserted between residues
 R;Shakhov, A.N.; Kuprash, D.V.; Aizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
 A;Reference number: JH0309; MUID:91065534; PMID:2249779
 A;Accession: JS0727
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-62, 'Q', 63-234 <SHA>
 A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
 C;Genetics:
 A;Introns: 62/3; 80/1; 96/1
 A;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
 F;1-81/Domain: propeptide #status predicted <PRO>
 F;82-234/Product: tumor necrosis factor #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;147-178/Disulfide bonds: #status predicted

Query Match 10.2%; Score 131.5; DB 1; Length 234;
 Best Local Similarity 22.9%; Pred. No. 0.00079;
 Matches 50; Conservative 36; Mismatches 79; Indels 53; Gaps 10;

QY 29 PNDSESNVPCWQKWLRLQKRLKMI-LRTSEETISVQEKQNIPLVREGRQVAAH 87
 DB 58 PQEESPN-----LHVPVQMVTLRSASRLSD-----KPL-----AH 93
 QY 88 ITGTGRGNTLSSPNSKNEKALGRKINSWSSRSGHSFLSNLHRLNGELVHEKGFYIY 147
 DB 94 VVA-----NPQVEQL-----QWLSQRANALLANGMKLTNQLVVPADGLIY 137
 QY 148 SQYFRFOEIKENTKNDKQMVYIKY-TSYDDPILLMKSARNCSWSDAEYV-----L 201
 DB 138 SQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNKNVLLSAIKSPCHRETPPEAEPMAY 192
 QY 202 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 238
 DB 193 EPIYLGGVFQLEKDRLLSTEVNQPEYLDLAESEQVIFG 230

RESULT 3
 S12606
 tumor necrosis factor alpha precursor - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C;Accession: S12606; S17290; S18965; I46659
 R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
 Nucleic Acids Res. 18, 5564, 1990
 A;Title: Gene sequence of porcine tumor necrosis factor alpha.
 A;Reference number: S12606; MUID:91016861; PMID:2216741
 A;Accession: S12606
 A;Molecule type: DNA
 A;Residues: 1-232 <DRE>
 A;Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
 R;Kuhnert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U.
 Gene 102, 171-178, 1991
 A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
 A;Reference number: S17289; MUID:91340150; PMID:1874444
 A;Accession: S17290
 A;Molecule type: DNA

A;Residues: 1-232 <KUH>
 A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
 A;Note: the authors translated the codon GAG for residue 202 as Gly
 R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
 submitted to the EMBL Data Library, January 1991
 A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis f
 A;Reference number: S18965
 A;Accession: S18965
 A;Molecule type: mRNA
 A;Residues: 1-232 <CHO>
 A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
 R;Pauli, U.; Beutler, B.; Peterhans, E.
 Gene 81, 185-191, 1989
 A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reactio
 A;Reference number: I46659; MUID:90034181; PMID:2478420
 A;Accession: I46659
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: mRNA
 A;Residues: 44-232 <PAU>
 A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
 C;Genetics:
 A;Introns: 62/3; 78/1; 93/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr
 F;1-77/Domain: propeptide #status predicted <PRO>
 F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;144-176/Disulfide bonds: #status predicted

Query Match 10.1%; Score 130; DB 1; Length 232;
 Best Local Similarity 25.1%; Pred. No. 0.0011;
 Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;

QY 80 GPORVAAHITGRGNTLSSPNS---KNEKALGRKINSWSSRSGHSFLSNLHRLNGEL 136
 DB 66 GLSLINPLAQGLRSSQTSQDKPAHVAVNVKAEGL--QWQSGYANALLANGVKLKDNGI 123
 QY 137 VTHEKGFYIYQTVFRFOEIKEN---TKNDKQMVYIYKTSYDPDPILLMKSARNCSW 193
 DB 124 VVPTDGLYLYSQVLFRGQCPSTNVLHTHTSRIA-----VSQTKVNLLSAISKSPQ 177
 QY 194 SK-----DAEYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-PFG 238
 DB 178 RETPEGAEAKPWEPIYLGGVFQLEKDRLLSAEINLPDYLDFAESGQVYFG 228

RESULT 4
 S15490
 tumor necrosis factor alpha precursor - white-footed mouse
 C;Species: Peromyscus leucopus (white-footed mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
 C;Accession: I54490
 R;Crew, M.D.; Filipovsky, M.E.
 Immunogenetics 35, 351-353, 1992
 A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu
 A;Reference number: I54490; MUID:92218012; PMID:1348497
 A;Accession: I54490
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-235 <RES>
 A;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
 C;Genetics:
 A;Gene: PLTNF
 A;Introns: 62/3; 81/1; 97/1
 C;Superfamily: tumor necrosis factor
 C;Keywords: glycoprotein; lipoprotein; myristylation
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 10.1%; Score 129.5; DB 2; Length 235;
 Best Local Similarity 24.5%; Pred. No. 0.0012;
 Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

A;Residues: 1-62, 'S', 64-233 <WAN>

178 YDPFILLMKSAKRNCSWK-----DAEYGYSYIVQGGIFELKENDRNFVSVTNHLLIDMDH 232
N:N:
163 YQTKNTLLSIAIKSPCORETPEGAEEKPMYEPIYLGVGFLQEKGRLSAEINRPDYLDFAE 222
:
233 EAS-FRG 238
: |||
223 SQGVYFG 229

RESULT 8
QMFXUJ
Lymphotoxin alpha precursor - human
N:Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence.revision 07-Jul-1995 #text.change 16-Jun-2000
A:Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A01645; A2
R:Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel
J. Cell. Biochem. 29, 171-181, 1985
A:Title: Structure and chromosomal localization of the human lymphotoxin gene.
A:Reference number: A92755; MUID:86086150; PMID:3001109
A:Accession: A92755
A:Molecule type: DNA
A:Residues: 1-59, 'N', 61-205 <NEB>
R:Iris, F.J.M.; Souguelret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurk
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within
A:Reference number: S36152; MUID:93272029; PMID:18499947
A:Accession: S36154
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-12, 'R', 14-205 <IRI>
A:Cross-references: EMBL:Z15026; NID:937211; PIDN:CAA78746.1; PID:G37213
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A:Title: Haplotypic polymorphisms of the TNFB gene.
A:Reference number: I54482; MUID:91139175; PMID:1671667
A:Accession: I54482
A>Status: translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-124, 'P', 126-205 <RES>
A:Cross-references: GB:M55913; NID:G339742; PIDN:AAB59455.1; PID:G339743
A:Experimental source: ancestral haplotype 57.1
A>Note: 59-Asn was also found (ancestral haplotype 8.1)
R:Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Brington, T.S.; Henzel, W.J.; Jarrett, J.A.
Nature 312, 721-724, 1984
A:Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour
A:Reference number: A93350; MUID:85086243; PMID:6334807
A:Accession: A93350
A:Molecule type: mRNA
A:Residues: 1-205 <GRA>
A:Cross-references: GB:X01393; NID:G34444; PIDN:CAA25649.1; PID:G34445
A:Experimental source: lymphoblastoid cell line REMI-1788
R:Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.F.
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A:Title: Tumor necrosis factors: gene structure and biological activities.
A:Reference number: A32877; MUID:87217059; PMID:3472740
A:Accession: B32877
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 35-205 <GOE>
R:Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Biochem. 100, 727-733, 1986
A:Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell
A:Reference number: A91906; MUID:87057135; PMID:3536896
A:Accession: A91906
A:Molecule type: mRNA
A:Residues: 1-59, 'N', 61-205 <KOB>
A:Cross-references: GB:D00102; NID:G219913; PIDN:BAA00064.1; PID:G219914
A>Note: The authors translated the codon TAT for residue 156 as Thr and ACC for resid
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Maesaki, N.; Nakamura, K.I.;
Imvphokine Res. 7, 175-185, 1988

[illegible]

Search completed: March 23, 2004, 09:15:49
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:07:59 ; Search time 17 Seconds

(without alignments)

744.297 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSKGIACFL.....NEHLDMDEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 56376

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	12.4	174	1	TN15 HUMAN
2	159.5	12.4	240	1	TN14 HUMAN
3	152.5	11.8	239	1	TN14_MOUSE
4	136.5	10.6	235	1	TNFB_RABIT
5	134.5	10.5	204	1	TNFB_PIG
6	132.5	10.3	234	1	TNFA_CAVPO
7	130	10.1	232	1	TNFA_PIG
8	129.5	10.1	235	1	TNFA_PERLE
9	127.5	9.9	204	1	TNFB_BOVIN
10	126	9.8	234	1	TNFB_HORSE
11	125	9.7	233	1	TNFA_MARMO
12	123	9.6	233	1	TNFA_HUMAN
13	122.5	9.5	229	1	TNFA_CEREL
14	122	9.5	205	1	TNFB_HUMAN
15	122	9.5	232	1	TNFA_PANTR
16	121	9.4	235	1	TNFA_MOUSE
17	121	9.4	235	1	TNFA_RAT
18	120	9.3	205	1	TNFB_MARMO
19	120	9.3	233	1	TNFA_PAPSP
20	118	9.2	233	1	TNFA_TURTR
21	117.5	9.1	201	1	TNFB_MACEU
22	117.5	9.1	234	1	TNFB_SHEEP
23	117	9.1	233	1	TNFA_MACMU
24	117	9.1	233	1	TNFA_PAPHU
25	116.5	9.1	233	1	TNFA_CANFA
26	116	9.0	233	1	TNFA_MACFA
27	116	9.0	233	1	TNFA_SAISC
28	114	8.9	202	1	TNFB_MOUSE
29	113.5	8.8	233	1	TNFA_TRIVU
30	113.5	8.8	234	1	TNFA_BOVIN
31	113	8.8	233	1	TNFA_BOVIN
32	113	8.8	233	1	TNFA_BURBU
33	113	8.8	233	1	TNFA_LANGL

RESULT 1

TN15_HUMAN ID	TN15_HUMAN STANDARD;	PRT;	174 AA.
AC	O95150;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).		
GN	TNFSF15 OR VEGI OR TNF1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Umbilical vein;		
RX	MEDLINE=99091541; PubMed=9872942;		
RA	Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,		
RA	Janat F., Kozak D., Xu S., Rojase L., Aggarwal B.B., Ruben S.,		
RA	Li L.-Y., Gentz R., Yu G.-L.;		
RT	"VEGI", a novel cytokine of the tumor necrosis factor family, is an		
RT	angiogenesis inhibitor that suppresses the growth of colon carcinomas		
RT	in vivo."		
RL	FASEB J. 13:181-189(1999).		
CC	-!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis		
CC	(in vitro).		
CC	-!- SUBUNIT: Homotrimer (Potential).		
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).		
CC	-!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.		
CC	Detected in placenta, lung, kidney, skeletal muscle, pancreas,		
CC	spleen, prostate, small intestine and colon.		
CC	-!- SIMILARITY: Belongs to the tumor necrosis factor family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF039390; RAD08783.1; -		
DR	HSSP; P50591; IDOG.		
DR	Genew; HGNC:11931; TNFSF15.		
DR	MIM; 604052; -		
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.		
DR	GO; GO:0005102; F:receptor binding; TAS.		
DR	GO; GO:0000074; P:regulation of cell cycle; TAS.		
DR	GO; GO:0000074; P:regulation of cell cycle; TAS.		
DR	InterPro; IPR006053; TNF-abc.		
DR	InterPro; IPR006052; TNF family.		
DR	InterPro; IPR008983; TNF-like.		
DR	InterPro; IPR003636; TNF_subf.		
DR	Pfam; PF00229; TNF; 1.		
DR	PRINTS; PR01234; TNFECROSISFCT.		
DR	ProDom; PD002012; TNF_subf; 1.		

ALIGNMENTS

DR SMART: SMO0207; TNF; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1 12
 FT TRANSMEM 13 25
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL)
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 26 174
 FT DISULFID 85 125
 FT CARBOHYD 56 56
 FT CARBOHYD 152 152
 FT CARBOHYD 152 152
 SQ SEQUENCE 174 AA; CCB83BA7EE673B98 CRC64;
 Query Match 12.4%; Score 160; DB 1; Length 174;
 Best Local Similarity 35.3%; Pred. No. 2.5e-06;
 Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;
 QY 116 WESSRSGHSLN-LHLRNGELVHEKGFYIYSQTYFRFQ-----EIKENTKDK-QM 168
 Db 42 WE-HELGLATKRMVNTNFKLLIPESGDYFIYSQTYFRGWTSECSIRAGRNKPDISI 100
 QY 169 VQIYKKT-SYDPDILLMKARNCSWKDAEYG---LYSYQGIFLKNDRIFVSVTN 224
 Db 101 TVVITKVTDSYPETQLMGTSVC-----EVGSNWFQPIYLGAMFSLQSGDKLMNVSD 155
 QY 225 EHLIDMDHE-ASRFGAEIV 242
 Db 156 ISLVDTYTKDKTFPGALL 174

RESULT 2
 TN14 HUMAN
 ID TN14 HUMAN STANDARD; Q8WVF8; Q96L22; PRT; 240 AA.
 AC Q8357; Q75476; Q8WVF8; Q96L22;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
 mediator-ligand) (HVEM-L).
 GN TNFSF14 OR LIGHT OR HVEM-L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=98122340; PubMed=9462508;
 RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
 RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
 RA Ware C.F.;
 RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
 RT ligands for herpesvirus entry mediator."
 RL Immunity 8:21-30(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RX MEDLINE=98438532; PubMed=9765287;
 RA Haripo J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
 RA Tan K.B., Dede K., Spanpanato J., Silverman C., Hensley P.,
 RA DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
 RA Truneh A., Young P.R.;
 RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
 RT HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
 RT growth."
 RL J. Biol. Chem. 273:27548-27556(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
 RX MEDLINE=21528948; PubMed=11673523;
 RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
 RT "Genomic characterization of LIGHT reveals linkage to an immune
 RT response locus on chromosome 19p13.3 and distinct isoforms generated
 RT by alternate splicing or proteolysis."
 RL J. Immunol. 167:5122-5128(2001).
 RN [4]

SEQUENCE FROM N.A.
 TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shmolen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
 CC decoy receptor TNFRSF6B modulates its effects. Activates NFkB,
 CC stimulates the proliferation of T cells, and inhibits growth of
 CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
 CC virus.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoform 1); Cytoplasmic (isoform 2).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O43557-1; Sequence=Displayed;
 CC Name=2; Synonyms=LIGHT delta-TM;
 CC IsoId=O43557-2; Sequence=VSP_006452;
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
 CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
 CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
 CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
 CC NONHEMATOPOIETIC TUMOR LINES.
 CC -!- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
 CC frameshift in position 178.
 CC -----
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 CC -----
 CC EMBL; AF036581; AAC39563.1; -;
 CC EMBL; AF064090; AAC25169.1; -;
 CC EMBL; AY028261; AAK26160.1; -;
 CC EMBL; BC018058; AAH18058.1; ALT_FRAME.
 CC HSSP; P01375; 4TSV.
 CC Genew; HGNC:11930; TNFSF14.
 CC MIM; 604520; -;
 CC GO; GO:0005102; F:receptor binding; TAS.
 CC GO; GO:0006917; P:induction of apoptosis; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR006053; TNF abc.
 CC InterPro; IPR006052; TNF family.
 CC InterPro; IPR008983; TNF like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF; 1.

TNFA_RABBIT
ID TNFA_RABBIT STANDARD; PRT; 235 AA.
AC P04924;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91065534; PubMed=2249779;
RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA Nedospasov S.A.;
RT "Structural analysis of the rabbit TNF locus, containing the genes
RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT factor).";
RL Gene 95:215-221(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219712; PubMed=3519138;
RA Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
RA Wallace R.B.;
RT "Molecular cloning of the gene encoding rabbit tumor necrosis
RT factor.";
RL DNA 5:157-165(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219711; PubMed=3519137;
RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
RA Hayashi H., Kato M., Seko M.;
RT "Molecular cloning and expression in Escherichia coli of the cDNA
RT coding for rabbit tumor necrosis factor.";
RL DNA 5:143-155(1986).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC EMBL; M12845; AAA31486.1; -
CC EMBL; M12846; AAA31482.1; -
CC EMBL; M60340; AAA31484.1; -
CC PIR; A25454; A25451.
CC HSSP; P06804; 2TNF.
CC InterPro; IPR006053; TNF_abc.

DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 235
FT CHAIN 80 235
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 235
FT SITE 79 90
FT MOD_RES 2 2
FT DISULFID 148 179
FT CONFLICT 63 63
FT CONFLICT 63 63
SQ SEQUENCE 235 AA; 25816 MW; 610177D0BD2EF871 CRC64;
Query Match 10.6%; Score 136.5; DB 1; Length 235;
Best Local Similarity 23.0%; Pred. No. 0.00032;
Matches 42; Conservative 37; Mismatches 81; Indels 23; Gaps 7;
QY 72 IGPLVERGQPVAAHITCTGRSNTL-SPNSKNEKALGRKINS-----WESSRSRG 122
Db 56 IGQEEEQSPNNL--HLVNPVQAVMTLRASRALSCKPLAHVVPVQVQEGQLQWLSQRAN 113
QY 123 HSFLSNLHRLNGELVHEKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKY-TSYDDP 181
Db 114 ALLANGMKUTDNLQVVPADGLYIYSQVLFSGO-----GCRSYVLLTHTVSFAVSYPNK 168
QY 182 ILLMKARNSCWSKDAEYG-----LYSIYOGGFFELKENDRIFVSVTNEHLIDMDHEAS- 235
Db 169 VNLISAISPCCHRETPPEAEPMWVPIYLGGVQLEKGDRLSTEVNQPEYLDLAESQV 228
QY 236 FFG 238
Db 229 YFG 231
RESULT 5
TNFB_PIG STANDARD; PRT; 204 AA.
AC P26445;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE factor ligand superfamily member 1).
GN LTA OR TNFSF1 OR TNFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9923;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91340150; PubMed=1874444;
RA Kuhnert P., Wuthrich C., Peterhans E., Pauli U.;
RT "The porcine tumor necrosis factor-encoding genes: sequence and
RT comparative analysis.";
RL Gene 102:171-178(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=large white; TISSUE=Fibroblast;
RX MEDLINE=21108615; PubMed=11169259;
RA Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
RA Renard C.;
RT "Sequence of the swine major histocompatibility complex region
RT containing all non-classical class I genes.";

```
RL Tissue Antigens 57:55-65(2001).
CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers) (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X54859; CAA38638.1; -.
CC EMBL; AJ251914; CAB63853.1; -.
CC PIR; S17289; S17289.
CC HSSP; P01374; 1TNF.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNCRSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS00049; TNF 2; 1.
CC Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 33
CC CHAIN 34 204 LYMPHOTOXIN-ALPHA.
CC CARBOHYD 95 95 N-LINKED (GLCNAC... ) (POTENTIAL).
CC SEQUENCE 204 AA; 21960 MW; 81263187435E56AC CRC64;
CC
CC Query Match 10.5%; Score 134.5; DB 1; Length 204;
CC Best Local Similarity 24.7%; Pred. No. 0.00039;
CC Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;
CC
CC QY 63 STVEQKQNSPLVRGPFQVAHITG-----TGRSNTLSSPNSKNEKALGRKINS 115
CC Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 42 SAAQPAHQH-PPKHLARGTLKPAHLVGDPTDPSLRWRANT-----DRAFLA--- 88
CC
CC QY 116 WESSRSGHSLNLHRLNGELVIEKGFYIYSQTYFRQEEIKENTKDKOMQVVIYKY 175
CC Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 89 -----HGFL-----LSNNSLAVPTSLGLYFVYSQVYFSGCGCPKATPTPLVLAHEVQLE 137
CC
CC QY 176 TS-YDPFILLMKSARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
CC Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CC 138 SSQYPPHVLSSAQKSCVCPQCPWP-VRSVYQGVAVFLIQDQLSTHTDGTTHLLSPSS 196
CC
CC QY 235 SFFGAF 240
CC Db | | | | |
CC 197 VFFGAF 202
CC
CC RESULT 6
CC TNFA-CAVPO
CC ID TNFA-CAVPO STANDARD; PRT; 234 AA.
CC AC P51435;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
CC ligand superfamily member 2) (TNF-a) (Cachectin).
CC GN TNF OR TNFSF2 OR TNFA.
CC OS Cavia porcellus (Guinea pig).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]_TaxID=10141;
RN SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RT "Cloning and characterisation of guinea pig TNF-alpha cDNA.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Dunkin-Hartley;
RX MEDLINE=97462215; PubMed=9316485;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:1524-1530(1997).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U39839; AAB06492.1; -.
CC EMBL; U77036; AAB19210.1; -.
CC HSSP; P06804; 2TNF.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNCRSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF 1; 1.
CC PROSITE; PS00049; TNF 2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
CC CHAIN 1 234
CC DOMAIN 80 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
CC FT CHAIN 1 35 CYTOLASMIC (POTENTIAL).
CC FT DOMAIN 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT TRANSMEM 36 56 (POTENTIAL).
CC FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
CC FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
CC FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
CC FT DISULFID 147 178 BY SIMILARITY.
CC SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;
CC
CC Query Match 10.3%; Score 132.5; DB 1; Length 234;
CC Best Local Similarity 24.6%; Pred. No. 0.00068;
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Matches 44; Conservative 33; Mismatches 77; Indels 25; Gaps 7;
QY 80 GPOVAAHTGT--RGRSNTL---SSPNSXNEKALGRKINS-----WESSRSGHSFL 126
Db 57 GPOREQFSGPPFRPLAQTLLRSASQNDNDFVAHVANQAEBELQWLSKRNALLA 116
QY 127 SNLHNLNGELVIEHKEFYIYSQTYFRFQEEIKENTKNDKQVQYIYKY-TSPDPILLM 185
Db 117 NGMLSDNQLWPSDGLYLYISQVLFKQ-----GCPSYLLTHTVSRLAVSYPEKVNLL 171
QY 186 KSARNCSWCKDAEYGV-----LYSIYGGIFELKENDRIFVSVTNEHLIDM-DHEASFFG 238
Db 172 SAKSPCKETPGEARKPWEPIYLGVEFQKGRDLRSAEVNLPOYLFADSGQIYFG 230

RESULT 7
TNFA_PIG STANDARD; PRT; 232 AA.
AC P23583;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91016861; PubMed=2216741;
RA Drews R.F., Coffee B.W., Prestwood A.K., McGraw R.A.;
RT "Gene sequence of porcine tumor necrosis factor alpha.";
RL Nucleic Acids Res. 18:5564-5564 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340150; PubMed=1874444;
RA Kuhnert P., Wuehrich C., Peterhans E., Pauli U.;
RT "The porcine tumor necrosis factor-encoding genes: sequence and
RT comparative analysis.";
RL Gene 102:171-178 (1991).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Macrophage;
RA Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;
RT "Complete nucleotide sequence of a cDNA encoding porcine tumor
RT necrosis factor-alpha.";
RL Anim. Biotechnol. 2:97-105 (1991).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Large white; TISSUE=Fibroblast;
RX MEDLINE=21108615; PubMed=11169259;
RA Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Valman M.,
RA Renard C.;
RT "Sequence of the swine major histocompatibility complex region
RT containing all non-classical class I genes.";
RL Tissue Antigens 57:55-65 (2001).
RN [5]
RP SEQUENCE OF 44-232 FROM N.A.
RX MEDLINE=90034181; PubMed=2478420;
RA Pauli U., Beutler B., Peterhans E.;
RT "Porcine tumor necrosis factor alpha: cloning with the polymerase
RT chain reaction and determination of the nucleotide sequence.";
RL Gene 81:185-191 (1989).
CC CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.

```

```

CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; X54001; CAA37949.1; -
CC EMBL; X54859; CAA38639.1; -
CC EMBL; X57321; CAA40591.1; -
CC EMBL; AJ251914; CAB63852.1; -
CC EMBL; M29079; AAA31128.1; -
CC PIR; S12606; S12606.
CC HSSP; P01375; 4TSV.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 232 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 232 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 57 232 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 144 176 BY SIMILARITY.
SQ SEQUENCE 232 AA; 25254 MW; 65E28F702D99C8BE CRC64;
Query Match 10.1%; Score 130; DB 1; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.0011;
Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;
QY 80 GPOVAAHTGTGRGNTLSSPNS---XNEKALGRKINSWESSRSGHSFLSNHLNGL 136
Db 66 GPLSINFLAQGRSSQTSDEKPAHVANVKAEGQL--QWQSGYANALLANGVKLNQL 123
QY 137 VIHEKGFYIYSQTYFRFOEIKEN---TKNDKQVQIYKYTSYDPDILLMKARNSCW 193
Db 124 VVPTDGLYLYISQVLFRCGCPSTNVLTHTSRIA-----VSQTKVNLSAIKSPCQ 177
QY 194 SK-----DAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
Db 178 RETPEGAEPKWPYEPIYLGVEFQLEKDRLSAEINLPDYLDPAESGQVYFG 228
RESULT 8
TNFA_PERLE STANDARD; PRT; 235 AA.
AC P36939;
DT 01-JUN-1994 (Rel. 29, Created)

```


DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (TNF-a) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Peromyscus leucopus (White-footed mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TaxID=10041;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92218012; PubMed=1348497;
 RA Crew M.D., Filipowski M.E.;
 RT "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
 RT Peromyscus leucopus (family Cricetidae).";
 RL Immunogenetics 35:351-353(1992).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
 CC cancer and infection, and is characterized by general ill health
 CC and malnutrition.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 CC EMBL; M59233; AAA40596.1; -
 CC F1R; I54490; I54490.
 CC HSP; P06804; 2TNF.
 CC InterPro; IPR006053; TNF abc.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008983; TNF_like.
 CC Pfam; PF00229; TNF; 1.
 CC PRINTS; PR01234; TNECROSISFCT.
 CC ProDom; PD002012; TNF_subf; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; 1.
 CC PROSITE; PS0049; TNF_2; 1.
 CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).
 FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 148 179 BY SIMILARITY.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 235 AA; 25822 MW; 235A5CF9F9AC624 CRC64;

Query Match 10.1%; Score 129.5; DB 1; Length 235;

Best Local Similarity 24.5%; Pred. No. 0.0012;
 Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;
 QY 72 ISPLVREGRGQVAAHITGRGSRNTL--SSPNSKNEKALGRKINSWE-----SRSCH 123
 DB 56 IGQREKEFPNNLP--IGSMAQTLLTRSSSQSSDKPVAHVYVANHCVDEQLWLSRGAN 113
 QY 124 SFLSN-LHLRNGELVTHKGFYIVYSQTYFRFOEIKENTKNDKQMVQVIYKY-TSYDDP 181
 DB 114 AULANGMDLKDNLVLPADGLVIVISQVLFKGQ-----GCSSVVLTHVSRFAVYEDK 168
 QY 182 IILMKSARNSCWSKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
 DB 169 VALLSAIKSPC-PKETPEGSELKPWEPIYVGGVQLEKGRDLSEAVNLPKYLDFAESGQ 227
 QY 236 -PRG 238
 DB 228 VYFG 231
 RESULT 9
 ID TNFB_BOVIN STANDARD; PRT; 204 AA.
 AC Q06600;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lymphotoxin-alpha precursor (Lr-alpha) (TNF-beta) (Tumor necrosis
 DE factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94083525; PubMed=8260599;
 RA Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
 RT "Cloning and characterization of the tandemly arranged bovine
 RT lymphotoxin and tumour necrosis factor-alpha genes.";
 RL Cytokine 5:336-341(1993).
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
 CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
 CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
 CC produced by lymphocytes and cytotoxic for a wide range of tumor
 CC cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
 CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
 CC associated (heterotrimers) (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 CC EMBL; Z14137; CAA78510.1; -
 CC F1R; I46046; S24641.
 CC HSP; P01374; 1TNF.
 CC InterPro; IPR006053; TNF abc.
 CC InterPro; IPR006052; TNF_family.
 CC InterPro; IPR008983; TNF_like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF; 1.
 CC PRINTS; PR01234; TNECROSISFCT.
 CC ProDom; PD002012; TNF_subf; 1.
 CC SMART; SM00207; TNF; 1.

RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 RT homology and chromosomal localization.";
 RL Nucleic Acids Res. 13:6361-6373(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85142190; PubMed=3856324;
 RA Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,
 RA van Arsdell J.N., Yamamoto R., Mark D.F.;
 RA "Molecular cloning of the complementary DNA for human tumor necrosis
 RT factor.";
 RL Science 228:149-154(1985).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86030296; PubMed=3932069;
 RA Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
 RA Kawashima E., Shaw A., Bougueleret L., Prieur S., Semon D., Mueller R.,
 RA Ruysschaert M.R., van Vliet A., Fiers W.;
 RA "Molecular cloning and expression of human tumor necrosis factor and
 RT comparison with mouse tumor necrosis factor.";
 RL Eur. J. Biochem. 152:515-522(1985).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
 RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
 RA Cohen D.;
 RA "Dense Ali clustering and a potential new member of the NF kappa B
 RT family within a 90 kilobase HLA class III segment.";
 RL Nat. Genet. 3:137-145(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Neville M.J., Milner C.M., Campbell R.D.;
 RA "A new member of the immunoglobulin superfamily and a V-ATPase G
 RT subunit are amongst the predicted products of novel genes close to the
 RT TNF locus in the human MHC.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
 RA Lasky S., Hood L.;
 RA "Sequence of the human major histocompatibility complex class III
 RT region.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Shina S., Tamiya G., Oka A., Inoko H.;
 RA "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Shina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
 RA "Genome diversity in HLA: a new strategy for detection of genetic
 RT polymorphisms in expressed genes within the HLA class III and class I
 RT regions.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Rieder M.J., Carrington D.P., Lee K.L., Livingston R.J., Daniels M.R.,
 RA Montoya M.A., Chung M.-W., Yi Q., Miyamoto K.E., Nguyen C.P.,
 RA Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
 RA Sherwood J.K., Wiltrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327029; PubMed=8499947;
 RA Tissue=Blood;
 RC Tissue=Blood;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [14]
 RP SEQUENCE OF 77-233 FROM N.A.
 RA Jiang J.S., Kim B.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE OF 84-214 FROM N.A.
 RA Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP PHOSPHORYLATION (MEMBRANE FORM).
 RX MEDLINE=96170872; PubMed=8597870;
 RA Pocik E., Duda E., Wallach D.;
 RA "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
 RT transfected HeLa cells.";
 RL J. Inflamm. 45:152-160(1995).
 RN [17]
 RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
 RX MEDLINE=99221647; PubMed=10205166;
 RA Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
 RA Roufogalis B.D., Chaudhri G.;
 RA "A casein kinase I motif present in the cytoplasmic domain of members
 RT of the tumor necrosis factor ligand family is implicated in 'reverse
 RL signalling'.";
 RL EMBO J. 18:2119-2126(1999).
 RN [18]
 RP MUTAGENESIS.
 RX MEDLINE=91184128; PubMed=2009860;
 RA Ostade X.V., Tavernier J., Prange T., Fiers W.;
 RL "Localization of the active site of human tumor necrosis factor
 RT (hTNF) by mutational analysis.";
 RL EMBO J. 10:827-836(1991).
 RN [19]
 RP MYRISTOYLATION.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;
 RL "Myristyl acylation of the tumor necrosis factor alpha precursor on
 RT specific lysine residues.";
 RL J. Exp. Med. 176:1053-1062(1992).
 RN [20]
 RP CLEARANCE BY ADAM17.
 RX MEDLINE=97186575; PubMed=9034191;
 RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,
 RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
 RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,
 RA Mitchell J., Moyer M., Pahel G., Rocque W., Overton L.K., Schoenen F.,
 RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
 RT "Cloning of a disintegrin metalloproteinase that processes precursor
 RL tumour-necrosis factor-alpha.";
 RL Nature 385:733-736(1997).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=89159409; PubMed=2922050;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "Structure of tumor necrosis factor.";
 RL Nature 338:225-228(1989).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=91193276; PubMed=1964681;

RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "The structure of tumor necrosis factor -- implications for
 RL biological function.";
 RL J. Cell Sci. Suppl. 13:11-18 (1990).
 RN [23]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=90008932; PubMed=2551905;
 RA Eck M.J., Sprang S.R.;
 RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
 RT Implications for receptor binding.";
 RL J. Biol. Chem. 264:17595-17605 (1989).
 RN [24]

Query Match 9.6%; Score 123; DB 1; Length 233;
 Best Local Similarity 23.0%; Pred. No. 0.0041;
 Matches 43; Conservative 32; Mismatches 70; Indels 42; Gaps 8;

QY 80 GPOR-----VAHITGTRGNTLSSPSK-----NEKALGRKINSWESSRSGH 123
 DB 57 GPQREFFRDLISLPLAQVRSRT---PSDKPVAHVANPQAGQL--QWLNRANA 111
 QY 124 SFLSNLHRLNGELVHEKGFYIYISQTVFRFOEIEKNTKNDKQMVYIYKVT-----S 177
 DB 112 LLANGVELRDNLVVPSEGLYLIYSQVLFKQ-----GCPSTHVLTHITISIAVS 162
 QY 178 YDPILLMKASRNSKWSK-----DABYGLYSYQGGIFELKENDRIFVSVTNEHLMDH 232
 DB 163 YQTKVNLLSAISKPCQRETPEGAERKPYEPIYGLGVFQLEKGRLSAEINRPDYLDFAE 222
 QY 233 EAS-PFG 238
 DB 223 SQQVYFG 229

RESULT 13
 ID TNFA CEREL STANDARD; PRT; 229 AA.
 AC P51743;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (TNF-a) (Cachectin) (Fragment).
 GN TNF OR TNFSF2 OR TNFA.
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lockhart E.A.;
 RT "Cloning and sequencing of cervine tumor necrosis factor.";
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
 CC cancer and infection, and is characterized by general ill health
 CC and malnutrition.

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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 CC -----
 DR EMBL; U14683; AAA50759.1; -;
 DR HSSP; P01375; 4TSV.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1
 DR PRINTS; PR01234; TNFCROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 KW Cytokine; Transmembrane; Signal-anchor.
 FT NON_TER 1
 FT CHAIN <1 229 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 74 229 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN <1 30 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 31 51 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 52 229 EXTRACELLULAR (POTENTIAL).
 FT SITE 72 73 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT DISULFID 141 173 BY SIMILARITY.
 SQ SEQUENCE 229 AA; 24987 MW; 16DE5F7AA5A7DB35 CRC64;

Query Match 9.5%; Score 122.5; DB 1; Length 229;
 Best Local Similarity 22.8%; Pred. No. 0.0044;
 Matches 41; Conservative 35; Mismatches 77; Indels 27; Gaps 7;

QY 80 GPQVAAHITGRGSRNTLSSPSKNEKALGR-----KINS-----WESSRSGHSFLS 127
 DB 52 GPQREEQPTGLSINSPLVQLTRSSQASINKPVAHVANINAQQLMLDSCANALWAN 111
 QY 128 NLHLRANGELVHEKGFYIYISQTVFRFOEIEKNTKNDKQMVYIYK--YTSYDPIILM 185
 DB 112 GVKLEDNLVVPDGLYLIYSQVLFKQ-----SCPSTPLFTHITISIAVSOTKVNIL 166
 QY 186 KSARNSC-----WSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHEAS-PFG 238
 DB 167 SAIXSPCHRETPWA-EAKPWYEPYQGVFQLEKGRLSAEINLPDYLDVAESGQVYFG 225

RESULT 14
 ID TNFB HUMAN STANDARD; PRT; 205 AA.
 AC P01374; Q9UKS8;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
 DE factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87217060; PubMed=3555974;
 RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
 RA Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
 RA Filippov S.A., Bystron N.S., Bolydova E.F., Chuvpilo S.A.,
 RA Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;
 RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-

RT alpha) and lymphotoxin (TNF-beta) in the human genome.";
RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86086150; PubMed=30011109;
RA Nedwin G.E., Jarrett-Nedwin J., Smith D.H., Naylor S.L.,
RA Sakaguchi A.Y., Goeddel D.V., Gray P.W.;
RT "Structure and chromosomal localization of the human lymphotoxin
RT gene.";
RL J. Cell. Biochem. 29:171-181 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87057135; PubMed=3536896;
RA Kobayashi Y., Miyamoto D., Asada M., Obinata M., Osawa T.;
RT "Cloning and expression of human lymphotoxin mRNA derived from a
RT human T cell hybridoma.";
RL J. Biochem. 100:727-733 (1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85086243; PubMed=6334807;
RA Gray P.W., Agarwal B.B., Benton C.V., Brington T.S., Henzel W.J.,
RA Jarrett J.A., Leung D.W., Moffat B., Ng P., Svedersky L.P.,
RA Palladino M.A., Nedwin G.E.;
RT "Cloning and expression of cDNA for human lymphotoxin, a lymphokine
RT with tumour necrosis activity.";
RL Nature 312:721-724 (1984).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92339500; PubMed=1353024;
RA Matsuyama N., Okawa N., Tsukii Y., Endo T., Kaji A.;
RT "Nucleotide sequence of a cDNA encoding human tumor necrosis factor
RT beta from B lymphoblastoid cell RPMI 1788.";
RL FEBS Lett. 302:141-144 (1992).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93372029; PubMed=8499947;
RA Iris F.J.M., Bouguerelet L., Prieur S., Caterina D., Primas G.,
RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
RA Cohen D.;
RT "Dense Alu clustering and a potential new member of the NF kappa B
RT family within a 90 kilobase HLA class III segment.";
RL Nat. Genet. 3:137-145 (1993).
RN [7]
RP SEQUENCE FROM N.A.
RA Neville M.J., Milner C.M., Campbell R.D.;
RT "A new member of the immunoglobulin superfamily and a V-ATPase G
RT subunit are amongst the predicted products of novel genes close to the
RT TNF locus in the human MHC.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Shiina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
RA Lasky S., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A., AND VARIANTS ARG-13; PRO-51 AND ASN-60.
RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND VARIANT ASN-60.
RX MEDLINE=93083656; PubMed=1451807;
RA Voigt C.G., Maurer-Fogy I., Adolf G.R.;
RT "Natural human tumor necrosis factor beta (lymphotoxin). Variable O-
RT glycosylation at Thr7, proteolytic processing, and allelic

RT variation.";
RL FEBS Lett. 314:85-88 (1992).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=92129275; PubMed=1733919;
RA Eck M.J., Ultsch M., Rinderknecht E., de Vos A.M., Sprang S.R.;
RT "The structure of human lymphotoxin (tumor necrosis factor-beta) at
RT 1.9-A resolution.";
RL J. Biol. Chem. 267:2119-2122 (1992).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 61-205 OF COMPLEX WITH
RP TNF1.
RX MEDLINE=93258809; PubMed=8387891;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445 (1993).
RN [14]
RP VARIANT ASN-60.
RX MEDLINE=91086846; PubMed=1670638;
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA Riethmuller G., Weiss E.H.;
RT "Polymorphic structure of the tumor necrosis factor (TNF) locus: an
RT NcoI polymorphism in the first intron of the human TNF-beta gene
RT correlates with a variant amino acid in position 26 and a reduced
RT level of TNF-beta production.";
RL J. Exp. Med. 173:209-219 (1991).
RN [15]
RP VARIANT PRO-125.
RX MEDLINE=91139175; PubMed=1671667;
RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT "Haplotypic polymorphisms of the TNF gene.";
RL Immunogenetics 33:50-53 (1991).
CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC TNFRSF1/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits.
CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; X01393; CAA25649.1; -
CC EMBL; X02911; CAA26670.1; -
CC EMBL; D00102; BAA00064.1; -
CC EMBL; M16441; BAA61199.1; -
CC EMBL; D12614; BAA02139.1; -
CC EMBL; M55913; AAB59455.1; -
CC EMBL; Z15026; CAA78746.1; -
CC EMBL; Y14768; CAA75071.1; -
CC EMBL; AF000505; BAB63397.1; -
CC EMBL; AF129756; AAD18092.1; -
CC EMBL; AY070490; AAL49956.1; -
CC EMBL; AY216498; AAO21135.1; -
CC EMBL; A06316; CAA00536.1; -
CC PIR; A92755; QMHUX.
CC PDB; 1TNR; 31-JUL-94.
CC GlycoSuiteDB; P01374; -
CC Genew; HGNC:6709; LTA.
CC MIM; 153440; -
CC GO; GO:0005102; F:receptor binding; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.

Query Match 9.5%; Score 122; DB 1; Length 232;
Best Local Similarity 22.3%; Pred. No. 0.0049;
Matches 41; Conservative 31; Mismatches 70; Indels 42; Gaps 7;

```

QY 72 ISPLVERGPQRY-----AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
Db 70 ISPLAQAGSSSRTPSKPVAHVVA-----NPQAEGL--QWLNERRANALLA 113
QY 127 SNHLRNGELVIEHKGFIYIYQTYFRFQBEIKENTKNDKQVQYIYKYT-----SYPD 180
Db 114 NGVELRDNQLVWPSGLYLIYSQVLFKQ-----GCPSTHVLTLTHTISRIAVSYQT 164
QY 181 PILLMKSARNSCWSK-----DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
Db 165 KVNLLSAIKSPCORETPEGAEAPWIEPIYLGGVFQLEKGRUSAEINRPDYLDFAESGQ 224
QY 236 -PFG 238
Db 225 VYFG 228

```

Search completed: March 23, 2004, 09:14:18
 Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 09:11:14 ; Search time 45 Seconds
(without alignments)
1703.798 Million cell updates/sec

Title: US-10-662-429-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYSKSGIACFL.....NEHLIDMDHEASFFGAFIVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 520272

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	305.5	23.7	214	13	Q9DDZ5
2	175.5	13.6	169	11	Q9WV90
3	157	12.2	154	6	Q8WJ19
4	151.5	11.8	227	13	Q7T2Q3
5	144.5	11.2	216	11	Q70332
6	141	11.0	231	13	Q8AW02
7	137.5	10.7	232	11	Q80XA4
8	135	10.5	156	11	Q91ZL4
9	135	10.5	215	6	Q9BEE8
10	135	10.5	217	11	Q9BERG
11	130.5	10.1	222	13	Q7T1U4
12	128	9.9	230	13	Q8JG37
13	126.5	9.8	225	13	Q8IB42
14	125	9.7	215	11	Q9BND1
15	124	9.6	216	6	Q9BEC4
16	123.5	9.6	216	6	Q9BEC9

17	122	9.5	205	4	Q8N4C3
18	121.5	9.4	225	13	Q9IB41
19	120	9.3	237	13	Q8AWC9
20	119	9.2	202	11	Q8OWE7
21	115.5	9.0	149	6	Q97543
22	110.5	8.6	217	6	Q9BEG0
23	110	8.5	93	6	Q9TTJ2
24	109.5	8.5	149	6	Q97538
25	109.5	8.5	149	6	Q9TTG8
26	108.5	8.4	214	6	Q9BEF3
27	108	8.4	103	6	Q864Y7
28	108	8.4	217	6	Q9BEG1
29	107	8.3	217	6	Q9BEF4
30	106.5	8.3	102	11	Q80Z06
31	105	8.2	138	6	Q9TTG7
32	103	8.0	216	6	Q9BEE0
33	99	7.7	217	6	Q9BEC5
34	98.5	7.7	102	11	Q80Z05
35	97.5	7.6	102	11	Q80Z04
36	97	7.5	174	4	Q8IZ15
37	97	7.5	208	4	Q8IZ16
38	93.5	7.3	102	11	Q80Z02
39	92.5	7.2	110	13	Q7ZZX5
40	92	7.1	103	6	Q864Z0
41	90.5	7.0	101	11	Q9R136
42	90.5	7.0	158	4	Q8IZ14
43	88.5	6.9	102	11	Q80Z03
44	85.5	6.6	240	13	Q800J1
45	83	6.4	163	16	Q8XLG9

ALIGNMENTS

RESULT 1

Q9DDZ5 PRELIMINARY; PRT; 214 AA.
AC Q9DDZ5
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE TRAIL-like protein.
GN TNFSF10L.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
ligands in the fish ovary."
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR EMBL; AF250041; AAG47640.1;
DR HSSP; P50591; 1D2Q.
DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; P550049; TNF 2; 1.
SQ SEQUENCE 214 AA, 24033 MW, 98C002474FF691AA CRC64;

Query Match: 23.7%; Score 305.5; DB 13; Length 214;
Best Local Similarity 37.6%; Pred. No. 1.1e-17;
Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps 3;

OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 ON NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Savan R., Sakai M.;
 RT "Cloning of tumor necrosis factor 3 alpha in carp."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB112424; BAC7690.1; --
 SQ SEQUENCE 227 AA; 23226 MW; 010BC2B1E8D7265E CRC64;

Query Match 11.8%; Score 151.5; DB 13; Length 227;
 Best Local Similarity 25.3%; Pred. No. 8.7e-05;
 Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7;

QY 75 LVPRGQPVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWSSRSGHSFSLNHLRNG 134
 DB 67 LSKENVTSKVAHLGSA-----YEPDVSKNIDWQONQDGAFFVSGGLKLVDR 113
 QY 135 ELVIHKGFFYIYSQTYFRFQBEIKENTKNDKQMVQVIYKTSYDP-----PILLMKSA 188
 DB 114 EIIIPNDGIVFIYSQVSFHI--SKNDMTEDQEVHSHAVFYSDFFGIYKP--LIRAA 169
 QY 189 RNSCW---SKDAEYGLSYIYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
 DB 170 RSACVHASNTEDVWD--TIYLGAFSLRAGDKLCTTTTELLPRVETDNAKTFEGVF 225

RESULT 5
 O70332 PRELIMINARY; PRT; 216 AA.
 AC O70332;
 DT 01-AUG-1998 (T-EMBLrel. 07, Created)
 DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Tumor necrosis factor-alpha (fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 ON NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA MEDLINE=98234044; PubMed=9573100;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 analysis of cytokine mRNA expression in experimental visceral
 leishmaniasis."
 RL Infect. Immun. 66:2135-2142(1998).
 DR EMBL: AF046215; AAC40100.1; --
 DR HSSP: P06804; 2TNF
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005164; P:tumor necrosis factor receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR006053; TNF abc.
 DR InterPro: IPR006052; TNF family.
 DR InterPro: IPR008983; TNF-like.
 DR InterPro: IPR003636; TNF_subf.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_subf; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 FT NON_TER 216
 SQ SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;

Query Match 11.2%; Score 144.5; DB 11; Length 216;

Best Local Similarity 26.9%; Pred. No. 0.00032;
 Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;

QY 80 GPQVAAH---ITGTRGRSNTL--SSPNSKNEKALGRKINS-----WSSRSGHSFSL 127
 DB 49 GPQREKFPNPIIGMGQTLTLRSSQNSNDKPGVHVANHQVVEQLEWLSHRANALLAN 108
 QY 128 NLHLRNGELVIHKGFFYIYSQTYFRFQBEIKENTKNDKQMVQVIYK-----YTSYDP 180
 DB 109 GMSLKDNLQIVPADGLYLVYSQVLRGQ-----GCPSYVLLTHVTSRIASVYED 157
 QY 181 PILLMKSAKNSCWSDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLID 229
 DB 158 NYNLLSAIKSPC-PKETPEGEELKPWYEFILYGVFQLEKGRLSAEVNLPKYLD 211

RESULT 6
 O8AW02 PRELIMINARY; PRT; 231 AA.
 AC O8AW02;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Putative tumour necrosis factor alpha two.
 GN TNF-ALPHA2PRO.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 ON NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,
 RA Wiegertjes G.F.;
 RT "Molecular and functional characterization of carp TNF: Association of
 TNF polymorphism with trypanotolerance."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ311801; CAC84642.2; --
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005164; P:tumor necrosis factor receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR006053; TNF abc.
 DR InterPro: IPR006052; TNF family.
 DR InterPro: IPR008983; TNF like.
 DR InterPro: IPR003636; TNF_subf.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_subf; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF 2; 1.
 SQ SEQUENCE 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;

Query Match 11.0%; Score 141; DB 13; Length 231;
 Best Local Similarity 23.3%; Pred. No. 0.00068;
 Matches 51; Conservative 38; Mismatches 90; Indels 40; Gaps 9;

QY 44 WLQRLVRRMILRTSEETISTVQEQQN-----ISPLVREGRQVAAHITGTR 92
 DB 29 WRVCGVLLAVALCAAAAVCFGLKSNQNGNALRLTLRDHLSENVTSKVAHLTGA- 87
 QY 93 GRSNTLSSPNSKNEKALGRKINSWSSRSGHSFSLNHLRNGELVIHKGFFYIYSQTYF 152
 DB 88 -----YDPDVCKDNL-----DWKQNDQAFVSGGLVLDREIIPNDGIFVYSQVSF 135
 QY 153 RFQBEIKENTKNDKQMV-----QYIKYTSYPPILLMKSAKNSC-WSKDAEYGLY-S 203
 DB 136 HI--SKDHMTEDQVVMHSHAVLRYSYSGYKP---LFSAIRSACVHASSEDLWYNT 190
 QY 204 IYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
 DB 191 IYLGAFNLRAEDRLRTETTKELLPRVSENGKTFEGVF 229

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RESULT 7
Q80XA4 Q80XA4 PRELIMINARY; PRT; 232 AA.
AC Q80XA4;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Tumor necrosis factor precursor (Fragment).
GN TNF.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
SEQUENCE FROM N.A.
RA Green R.M., Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse tumor necrosis factor gene.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY249143; AAP03078.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR006052; TNF_like.
DR InterPro; IPR008983; TNF_subf.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 232 AA; 25704 MW; E48A9379DB4F216D CRC64;

Query Match 10.7%; Score 137.5; DB 11; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.0013;
Matches 45; Conservative 36; Mismatches 78; Indels 25; Gaps 8;

Qy 72 ISPLVRRGCRQVAAHITGFRGRNTL-SSPNSKNEKALGRKINS-----WESSRSG 122
Db 56 IGPOREKFPNNLP--IGSMAQTLLRSQSSSDKPVAAHVAVHQAQVDSQLEWLSRRAN 113
Qy 123 HSFLSLNHLRNGELVIEHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKY--TSYPDP 181
Db 114 ALLANGMDLKNQVLVPADGLYLYVSQVLFKQKQ-----GCSNYVLLTHTVSRAVSVYEDK 168
Qy 182 ILLMKSARNCSWKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
Db 169 VLLLSAITSKSPC-PKETPGSELKPWYEPYILGVGVQLEKGRLSAEVNHLPKYLDFAESGQ 227
Qy 236 -FFG 238
Db 228 VYFG 231

RESULT 8
Q91ZL4 Q91ZL4 PRELIMINARY; PRT; 156 AA.
AC Q91ZL4;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.

Query Match 10.7%; Score 137.5; DB 11; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.0013;
Matches 45; Conservative 36; Mismatches 78; Indels 25; Gaps 8;

Qy 72 ISPLVRRGCRQVAAHITGFRGRNTL-SSPNSKNEKALGRKINS-----WESSRSG 122
Db 56 IGPOREKFPNNLP--IGSMAQTLLRSQSSSDKPVAAHVAVHQAQVDSQLEWLSRRAN 113
Qy 123 HSFLSLNHLRNGELVIEHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYKY--TSYPDP 181
Db 114 ALLANGMDLKNQVLVPADGLYLYVSQVLFKQKQ-----GCSNYVLLTHTVSRAVSVYEDK 168
Qy 182 ILLMKSARNCSWKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
Db 169 VLLLSAITSKSPC-PKETPGSELKPWYEPYILGVGVQLEKGRLSAEVNHLPKYLDFAESGQ 227
Qy 236 -FFG 238
Db 228 VYFG 231

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OX NCBI_TaxID=42415;
RN [1]
SEQUENCE FROM N.A.
RA Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421388; AAL18818.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C826E4 CRC64;

Query Match 10.5%; Score 135; DB 11; Length 156;
Best Local Similarity 23.5%; Pred. No. 0.0013;
Matches 43; Conservative 33; Mismatches 67; Indels 40; Gaps 8;

Qy 65 VQKQONISPLVRRGCRQVAAHITGFRGRNTLSSPNSKNEKALGRKINSWESSRSGHS 124
Db 1 LRSSSQNLSS-----DKPVAHVVA-----NQABEQL-----EWLSQRANAL 36
Qy 125 FLSNHLRNGELVIEHEKGFYIYSQTYFRFQBEIKENTKNDKQVQYIYK--YTSYPDPI 182
Db 37 LANGMDLRNNQVLVPADGLYLYVSQVLF-----KGLGRSNCCELLTHTVSRIAVSVYEDKV 90
Qy 183 ILLMKSARNCSWKDAEYG-----LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235
Db 91 VLLLSAITSKSPC-PKETPGSELKPWYEPYILGVGVQLEKGRLSAEVNHLPKYLDFAESGQV 149
Qy 236 FFG 238
Db 150 YFG 152

RESULT 9
Q9BE8 Q9BE8 PRELIMINARY; PRT; 215 AA.
AC Q9BE8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -.
DR HSP; P01375; 4TSV.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.

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DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR006053; TNF_family.
DR InterPro: IPR008983; TNF_like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 230 AA; 2559 MW; 3A40D391F75DB019 CRC64;

Query Match
Best Local Similarity 9.8%; Score 128; DB 13; Length 230;
Matches 37; Conservative 25; Mismatches 53; Indels 12; Gaps 5;

QY 124 SFLSNHLRNGELVIEHKGFFYIYSQYFRFQEEIKENTKNDKQMVQYIYKTSYDPPIL 183
D 104 SFSGLKLENEIKLRDGLYFVYSQASYRLCK-AGDETEGEVHMVKVSRWSDSYS 162
QY 184 -----LMSARNSCWSDAEGLY-----SIYGGIFELKENDRIFVSVTNEHLIDMCHEA-- 234
D 163 SWKPLLSATRSACKTTEYQKYWGAVYLGAALFKAGDRL-RTVMDEXLKPVESAGG 221
QY 235 -SPFGAF 240
D 222 KTFPGTF 228

RESULT 13
Q9IB42
ID Q9IB42 PRELIMINARY; PRT; 225 AA.
AC Q9IB42
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor.
OS Paralichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20491932; PubMed=11035080;
RA Harono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular Cloning, Characterization, and Expression of TNF cDNA and
RL J. Immunol. 165:4423-4427(2000).
DR EMBL: AB040448; BRA94969.1; -.
DR HSSP: P01375; 4TSV.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR006053; TNF_family.
DR InterPro: IPR008983; TNF_like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947B45FC82658 CRC64;

Query Match
Best Local Similarity 9.8%; Score 126.5; DB 13; Length 225;
Matches 42; Conservative 40; Mismatches 78; Indels 31; Gaps 8;

QY 67 EKQNISPLVVRGPQVAAHITGRGRSNTLSPNS---KNEKALGRKINSWESSRSGH 123

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Db 47 EXTEPHNTLRQISSRAAAHLEG-RDEDETSNKLVKNDGLA-----FTQGGF 98
QY 124 SFLSNHLRNGELVIEHKGFFYIYSQYFRFQ-----EEIKENTKNDKQMVQY-IYKYT 176
D 99 ELVDN-----HIIIPRSGLYFVYSQASFRVSCSSDDADDGKAAEKHLTISHRVWLT 152
QY 177 -SYDDPILLMKSARNSCWS-----KDAEYGLYSYIYGGIFELKENDRIFVSVTNEHLID 229
D 153 ESLGTQVSLMSAVRSACKSQSDAYRDGGQWYNAILGAVFQNLNEGDKLWTETNMLSELE 212
QY 230 MDHEASFFGAF 240
D 213 TSGKTFFGVF 223

RESULT 14
Q99ND1
ID Q99ND1 PRELIMINARY; PRT; 215 AA.
AC Q99ND1
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tamiasciurus hudsonicus (American red squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Tamiasciurus.
OX NCBI_TaxID=10009;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ286824; CAC28540.1; -.
DR HSSP: P06804; 2TNF.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR006053; TNF_family.
DR InterPro: IPR008983; TNF_like.
DR InterPro: IPR003636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match
Best Local Similarity 9.7%; Score 125; DB 11; Length 215;
Matches 35; Conservative 29; Mismatches 62; Indels 18; Gaps 4;

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D 71 SSSQNMNDKPVAVHVVANQTEQLQWLSRRANALLANGMELIDNLVVPADGLYIYSQVL 130
QY 152 FRFQEEIKENTKNDKQMVQYIYKY-TSYDPPILLMKSARNSCWSDAEGLYS-----IY 205
D 131 FKQG-----GCSSYVLLTHTVSRFAVSQDKYNLLSATKSPCKSLGAEKPKWYEPIY 185
QY 206 QGGIFELKENDRIFVSVTNEHLID 229
D 186 LGGVTELOKGRLSAEVNLPSYLD 209

RESULT 15

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Search completed: March 23, 2004, 09:15:15
Job time : 46 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:03 ; Search time 23 Seconds
(without alignments)
630.735 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGSGLGTCVLIV.....NEHLMDHREASFFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	US-08-670-354-2
2	1478	100.0	281	3	US-08-584-031-1
3	1478	100.0	281	3	US-08-780-496-1
4	1478	100.0	281	3	US-08-893-086-10
5	1478	100.0	281	3	US-08-320-424-2
6	1478	100.0	281	4	US-09-333-593A-6
7	1478	100.0	281	4	US-09-157-864-11
8	1478	100.0	281	4	US-09-825-563-2
9	1478	100.0	281	4	US-10-039-785-66
10	1478	100.0	281	5	PCT-US96-10895-2
11	1469	99.4	279	4	US-09-072-993C-3
12	988	66.8	253	3	US-09-320-424-11
13	988	66.8	253	4	US-09-825-563-11
14	988	66.8	256	3	US-09-320-424-13
15	988	66.8	256	4	US-09-825-563-13
16	930	62.9	177	3	US-09-105-343A-7
17	930	62.9	291	1	US-08-670-354-6
18	930	62.9	291	3	US-09-320-424-6
19	930	62.9	291	4	US-09-825-563-6
20	930	62.9	291	5	PCT-US96-10895-6
21	850	57.5	161	4	US-09-565-423-7
22	654	44.2	183	3	US-09-105-343A-8
23	482	32.6	101	1	US-08-670-354-4
24	482	32.6	101	3	US-09-320-424-4
25	482	32.6	101	4	US-09-825-563-4
26	482	32.6	101	5	PCT-US96-10895-4
27	446	30.2	85	4	US-09-632-287A-12

28 258.5 17.5 294 3 US-08-996-139-11 Sequence 11, Appl
29 258.5 17.5 294 3 US-08-995-659-11 Sequence 11, Appl
30 258.5 17.5 294 3 US-09-215-649A-11 Sequence 11, Appl
31 258.5 17.5 294 4 US-08-577-780-11 Sequence 11, Appl
32 258.5 17.5 294 4 US-09-577-800-11 Sequence 11, Appl
33 258.5 17.5 294 4 US-09-466-496-11 Sequence 11, Appl
34 258.5 17.5 294 4 US-09-871-856-11 Sequence 11, Appl
35 258.5 17.5 294 4 US-09-871-291-11 Sequence 11, Appl
36 258.5 17.5 294 4 US-09-877-650-11 Sequence 11, Appl
37 258.5 17.5 316 2 US-08-842-842-7 Sequence 7, Appl
38 258.5 17.5 316 3 US-08-989-362-2 Sequence 2, Appl
39 258.5 17.5 316 4 US-09-052-521C-2 Sequence 2, Appl
40 258.5 17.5 316 4 US-09-671-658A-2 Sequence 2, Appl
41 258.5 17.5 316 4 US-09-396-937-4 Sequence 4, Appl
42 258.5 17.5 316 4 US-09-396-937-6 Sequence 6, Appl
43 251.5 17.0 317 3 US-08-996-139-13 Sequence 13, Appl
44 251.5 17.0 317 3 US-08-995-659-13 Sequence 13, Appl
45 251.5 17.0 317 3 US-09-215-649A-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2
Query Match 100.0%; Score 1478; DB 1; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120

QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240

QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 2
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669-220S03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120

QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240

QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim

Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60
Db 1 MAMMEVGGPSLGTCVLIVFTVLLQSLCAVAVYVFTNELKQMDKYKSGIACFLKE 60

QY 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120
Db 61 DDSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONTSPILVRERGQ 120

QY 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180
Db 121 RVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSRSGHSFLSNHLRNGELVHEKG 180

QY 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240
Db 181 FYIYSQTYFRFQEEIKENTKNDKQVQYIKYTSYDPDILLMKSAARNCSWCKDAEYGLY 240

QY 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 4
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA

; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-3881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-780-496-1

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembek, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYVYFTNELKQMDKYSKSGIACFLKE 60
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Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 5
US-09-320-424-2
Sequence 2, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368

EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 281
TYPE: PRT
ORGANISM: human
US-09-320-424-2

Query Match 100.0%; Score 1478; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYVYFTNELKQMDKYSKSGIACFLKE 60
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Db 61 DSYWDPNDEESMNSPCWQVQKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
QY 181 FYYISQTYFRFOEIKENTKNDKQMVQYIYKYTSYPPDILLMKSNRSCWSDAEYGLY 240
Db 181 FYYISQTYFRFOEIKENTKNDKQMVQYIYKYTSYPPDILLMKSNRSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 6
US-09-333-593A-6
Sequence 6, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMSERED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 281
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-6

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVATYVYFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYDNDPDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVREGRGPQ 120
DB 61 DDSYDNDPDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVREGRGPQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSQDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSQDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

US-09-157-864-11
; Sequence 11, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSER: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-11

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
QY 61 DDSYDNDPDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVREGRGPQ 120
DB 61 DDSYDNDPDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVREGRGPQ 120

QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSQDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSQDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

US-09-825-563-2
; Sequence 2, Application US/098255563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-09-825-563-2

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.7e-149;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTVYFTNELKQMDKYSGSIACFLKE 60
QY 61 DDSYDNDPDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVREGRGPQ 120
DB 61 DDSYDNDPDEESMNSPCWQVKWQLRQLVRKMLRTSEETISTVQKQKQNIPLVREGRGPQ 120
QY 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
DB 121 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKG 180
QY 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSQDAEYGLY 240
DB 181 FYIYSQTYFRQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSAARNCSWKSQDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 9

US-10-039-785-66
; Sequence 66, Application US/10039785

Patent No. 6538938
 GENERAL INFORMATION:
 APPLICANT: Salcedo et al.
 TITLE OF INVENTION: Antibodies that Immunospesifically Bind to TRAIL
 TITLE OF INVENTION: Receptors
 FILE REFERENCE: PF550
 CURRENT APPLICATION NUMBER: US/10/039,785
 CURRENT FILING DATE: 2002-05-07
 PRIOR APPLICATION NUMBER: 60/369,860
 PRIOR FILING DATE: 2002-04-05
 PRIOR APPLICATION NUMBER: 60/341,237
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 60/331,310
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/331,044
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: 60/327,364
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: 60/323,807
 PRIOR FILING DATE: 2001-09-21
 PRIOR APPLICATION NUMBER: 60/309,176
 PRIOR FILING DATE: 2001-08-02
 PRIOR APPLICATION NUMBER: 60/294,981
 PRIOR FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: 60/293,473
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 66
 LENGTH: 281
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-039-785-66

Query Match 100.0%; Score 1478; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.7e-149;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAMMEVQGGPSLGQTCLVLI	FTVLLQSLCAVTVYVFTN	ELKQMDKYKSGIACFLKE	60
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QY	61	DDSYWDPNDEESNCPQWQ	KLQRLVRKMLRTSEETIS	TVQEKQONISPLVRRGPQ	120
Db	61	DDSYWDPNDEESNCPQWQ	KLQRLVRKMLRTSEETIS	TVQEKQONISPLVRRGPQ	120
QY	121	RVAAHITGTRGRSNTLSS	PNKNEKALGRKINSWESS	SRSGHSLNHLRNGELVH	180
Db	121	RVAAHITGTRGRSNTLSS	PNKNEKALGRKINSWESS	SRSGHSLNHLRNGELVH	180
QY	181	FYIYSQTYFRFOEIKENT	KNDKQWQVIYKYTSYPP	DPILLMKSARNSCWSDA	240
Db	181	FYIYSQTYFRFOEIKENT	KNDKQWQVIYKYTSYPP	DPILLMKSARNSCWSDA	240
QY	241	SIYQGGIFELKENDRIFV	SVTNEHLIDMDHEASFF	GAFVLG 281	
Db	241	SIYQGGIFELKENDRIFV	SVTNEHLIDMDHEASFF	GAFVLG 281	

RESULT 10
 PCT-US96-10895-2
 Sequence 2, Application PC/TUS9610895
 GENERAL INFORMATION:
 APPLICANT: Immunex Corporation.
 TITLE OF INVENTION: Cytokine That Induces Apoptosis
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.5.2
 SOFTWARE: Microsoft Word, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/10895
 FILING DATE: 25-JUN-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA: US 08/496,632
 FILING DATE: 29-JUN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA: US 08/548,368
 FILING DATE: 01-NOV-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2835-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-10895-2

Query Match 100.0%; Score 1478; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.7e-149;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAMMEVQGGPSLGQTCLVLI	FTVLLQSLCAVTVYVFTN	ELKQMDKYKSGIACFLKE	60
Db	1	MAMMEVQGGPSLGQTCLVLI	FTVLLQSLCAVTVYVFTN	ELKQMDKYKSGIACFLKE	60
QY	61	DDSYWDPNDEESNCPQWQ	KLQRLVRKMLRTSEETIS	TVQEKQONISPLVRRGPQ	120
Db	61	DDSYWDPNDEESNCPQWQ	KLQRLVRKMLRTSEETIS	TVQEKQONISPLVRRGPQ	120
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Db	121	RVAAHITGTRGRSNTLSS	PNKNEKALGRKINSWESS	SRSGHSLNHLRNGELVH	180
QY	181	FYIYSQTYFRFOEIKENT	KNDKQWQVIYKYTSYPP	DPILLMKSARNSCWSDA	240
Db	181	FYIYSQTYFRFOEIKENT	KNDKQWQVIYKYTSYPP	DPILLMKSARNSCWSDA	240
QY	241	SIYQGGIFELKENDRIFV	SVTNEHLIDMDHEASFF	GAFVLG 281	
Db	241	SIYQGGIFELKENDRIFV	SVTNEHLIDMDHEASFF	GAFVLG 281	

RESULT 11
 US-09-072-993C-3
 Sequence 3, Application US/09072993C
 Patent No. 6346388
 GENERAL INFORMATION:
 APPLICANT: Michael R. Brigham-Burke
 APPLICANT: Peter R. Young
 TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
 CURRENT APPLICATION NUMBER: US/09/072,993C
 FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/055,513
 PRIOR FILING DATE: 1997-08-13
 PRIOR APPLICATION NUMBER: 60/056,980

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; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3

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Best Local Similarity 99.4%; Score 1469; DB 4; Length 279;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MMEVGGPSLGGTCLVLIIVFTVLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKEDD 62
Db 1 MMEVGGPSLGGTCLVLIIVFTVLQSLCAVAVYVYFTNELKQMDKYSKSGIACFLKEDD 60

QY 63 SYWDPNDESMNSPCWQVKQWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGQPV 122
Db 61 SYWDPNDESMNSPCWQVKQWLQRLVRKMLRTSEETISTVQEKQONISPLVRERGQPV 120

QY 123 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKGFY 182
Db 121 AAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVIHEKGFY 180

QY 183 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYDPDPILLMKSARNCSKDAEYGLYSI 242
Db 181 YIYSQTYFRFOEIKENTKNDKQWQVYIYKTSYDPDPILLMKSARNCSKDAEYGLYSI 240

QY 243 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 YOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 279

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; EARLIER FILING DATE: 1999-05-26
; EARLIER FILING DATE: 1998-11-10
; EARLIER FILING DATE: 1998-03-26
; EARLIER FILING DATE: 1998-03-26
; EARLIER FILING DATE: 1996-06-25
; EARLIER FILING DATE: 1995-11-01
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match
Best Local Similarity 66.8%; Score 988; DB 3; Length 253;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVK---WQLRQLVRKMLRT 95
Db 29 SDRMKQIEDKI-----EEILSKIYHIENETARIKKLIGERTST 67

QY 96 SEETISTVQEKQONISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 155
Db 68 SEETISTVQEKQONISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 127

QY 156 SRSRSHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 215
Db 128 SRSRSHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 187

QY 216 YPDPIILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFF 275
Db 188 YPDPIILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFF 247

QY 276 GAFLVG 281
Db 248 GAFLVG 253

Query Match
Best Local Similarity 66.8%; Score 988; DB 4; Length 253;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDESMNSPCWQVK---WQLRQLVRKMLRT 95
Db 29 SDRMKQIEDKI-----EEILSKIYHIENETARIKKLIGERTST 67

QY 96 SEETISTVQEKQONISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 155
Db 68 SEETISTVQEKQONISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWE 127

QY 156 SRSRSHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 215
Db 128 SRSRSHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVYIYKTS 187

QY 216 YPDPIILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFF 275
Db 188 YPDPIILLMKSARNCSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFF 247

QY 276 GAFLVG 281
Db 248 GAFLVG 253
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:06:53 ; Search time 46 Seconds
(without alignments)

1581.879 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMBVQGGPSIGQTCVLIV.....NEHLMDHRAFFGAFILWG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 25895339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	1478	100.0	281	8	US-08-916-625B-6
2	1478	100.0	281	8	US-08-971-317A-8
3	1478	100.0	281	9	US-09-813-329-17
4	1478	100.0	281	9	US-09-193-663-8
5	1478	100.0	281	9	US-09-334-465-1
6	1478	100.0	281	10	US-09-919-039-118
7	1478	100.0	281	12	US-10-202-062-20
8	1478	100.0	281	12	US-10-662-429-2
9	1478	100.0	281	12	US-10-662-430-2
10	1478	100.0	281	12	US-10-662-431-2
11	1478	100.0	281	13	US-10-039-785-66
12	1478	100.0	281	13	US-10-011-125-4
13	1478	100.0	281	13	US-10-001-054-54
14	1478	100.0	281	14	US-10-093-766-54
15	1478	100.0	281	14	US-10-174-654-11

SUMMARIES

RESULT 1
US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication NO. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701

ALIGNMENTS

16	1478	100.0	281	14	US-10-151-882-41
17	1478	100.0	281	14	US-10-218-547-20
18	1478	100.0	281	14	US-10-322-673-72
19	1478	100.0	281	14	US-10-139-785-66
20	1478	100.0	281	14	US-10-310-793-26
21	1478	100.0	281	15	US-10-292-486-5
22	1478	100.0	281	15	US-10-333-712-1
23	1469	99.4	279	13	US-10-066-209-3
24	1269.5	85.9	246	9	US-09-855-544A-13
25	1017	68.8	208	9	US-09-855-544A-16
26	985.5	66.7	461	12	US-10-389-223A-6
27	982	66.4	480	12	US-10-389-223A-4
28	978	66.2	614	12	US-10-389-223A-2
29	964.5	65.3	296	14	US-10-185-425-5
30	937.5	63.4	188	9	US-09-855-544A-14
31	930	62.9	291	10	US-09-873-829-6
32	930	62.9	291	13	US-10-017-910-6
33	887	60.0	168	9	US-09-900-530A-10
34	878	59.4	166	9	US-09-779-050A-16
35	859	58.1	164	13	US-10-116-378-29
36	850	57.5	161	14	US-10-216-074-7
37	849	57.4	161	14	US-10-338-083-11
38	836	43.0	172	9	US-09-779-050A-17
39	561	38.0	113	9	US-09-855-544A-15
40	482	32.6	98	9	US-09-855-544A-9
41	468	31.7	88	9	US-09-855-544A-10
42	446	30.2	85	14	US-10-286-696-12
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44	258.5	17.5	294	9	US-09-871-856-11
45	258.5	17.5	294	9	US-09-877-650-11

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Sequence 72, Appl
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Sequence 17, Appl
Sequence 15, Appl
Sequence 10, Appl
Sequence 9, Appl
Sequence 12, Appl
Sequence 20, Appl
Sequence 11, Appl
Sequence 11, Appl

TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-625B-6
Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
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DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
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DB 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 2

US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8
Query Match 100.0%; Score 1478; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVWG 281

RESULT 3

US-09-813-329-17
; Sequence 17, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mol
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1478; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCAVAVTVYFTNKLKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
DB 61 DDSYWDPNDEESMNSPCQWKQLRQLVRKMLRTSEETISTVQEKQNIPLVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEBIKENTKNDKQVQYIYKYTSYPPDILLMKSARNCSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||

RESULT 4

US-09-193-663-8
 ; Sequence 8, Application US/09193663
 ; Patent No. US20020055624A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
 ; FILE REFERENCE: 6255.US.02
 ; CURRENT APPLICATION NUMBER: US/09/193,663
 ; CURRENT FILING DATE: 1998-11-17
 ; EARLIER APPLICATION NUMBER: 60/065,916
 ; EARLIER FILING DATE: 1997-11-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PseSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-193-663-8

Query Match 100.0%; Score 1478; DB 9; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 |||||
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 |||||
 QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKDAEYGLY 240
 |||||
 Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKDAEYGLY 240
 |||||

RESULT 5

US-09-934-465-1
 ; Sequence 1, Application US/09934465
 ; Patent No. US20020102233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: APO-2 LIGAND
 ; FILE REFERENCE: 11669.22US03
 ; CURRENT APPLICATION NUMBER: US/09/934,465
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: 08/584,031
 ; PRIOR FILING DATE: 1996-01-09
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-934-465-1

Query Match 100.0%; Score 1478; DB 9; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 |||||
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 |||||
 QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKDAEYGLY 240
 |||||
 Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKDAEYGLY 240
 |||||
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||

RESULT 6

US-09-919-039-118
 ; Sequence 118, Application US/09919039
 ; Publication No. US20030108871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 118
 ; LENGTH: 281
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030108871A1 0595090CD1
 ; US-09-919-039-118

Query Match 100.0%; Score 1478; DB 10; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 |||||
 Db 1 MAMMEVQGGPSLGQTCVLIVFTVLQSLCVAVTVYFTNELKQMDKYKSGIACFLKE 60
 |||||
 QY 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 Db 61 DDSYWDPNDEESMNSPCQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGQ 120
 |||||
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVTHEKG 180
 |||||
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKDAEYGLY 240
 |||||
 Db 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKTSYDPDPILLMKSARNCSWKDAEYGLY 240
 |||||
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 |||||

RESULT 7

US-10-202-062-20
 ; Sequence 20, Application US/10202062

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; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-10-202-062-20

Query Match      100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVYIKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQMVYIKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 9
US-10-662-429-2
; Sequence 2, Application US/10662430
; Publication No. US20040048340A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,430
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
; US-10-202-062-20

Query Match      100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCWQVKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
DB 61 DDSYWDPNDEESMNSPCWQVKQRLQRLVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQMVYIKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQMVYIKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281
DB 241 SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 8
US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
```

```

; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-430-2

Query Match      100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPILVRERGQ 120
DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPILVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281

RESULT 10
US-10-662-431-2
; Sequence 2, Application US/10662431
; Publication No. US20040047864A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/662,431
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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US-10-662-431-2

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Query Match      100.0%; Score 1478; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPILVRERGQ 120
DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPILVRERGQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSPLSNLHRLNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
DB 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKYTSYDPDPILLMKSGARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFSVTVNEHLIDMDHEASFFGAFLVG 281

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RESULT 11

```

US-10-039-785-66
; Sequence 66, Application US/10039785
; Publication No. US20020067846A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66

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Query Match      100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCAVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVKMLRTSEETISTVQEQQNISPILVRERGQ 120

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Db	61	DDSWDPNDESMSPCQVWKQLRVRKMLLR	TSSEITISIVQKQKQINISPLVRRGPQ	120
Qy	121	RVAAHITGTRGSRNTLSSPNSGKNEKALGRKINSWESSRGSHGFLSNLHLRNGELVIHEKG	180	
Db	121	RVAAHITGTRGSRNTLSSPNSGKNEKALGRKINSWESSRGSHGFLSNLHLRNGELVIHEKG	180	
Qy	181	PYYIYSQYFYRFOBEIKENTKNDKQMVQYIYKYTSYPPILLAMKARNWSCWKDAEYGLY	240	
Db	181	PYYIYSQYFYRFOBEIKENTKNDKQMVQYIYKYTSYPPILLAMKARNWSCWKDAEYGLY	240	
Qy	241	SIYOGIFELKENDRIFVSVTNHEHIDMDHEASFFGALVIG	281	
Db	241	SIYOGIFELKENDRIFVSVTNHEHIDMDHEASFFGALVIG	281	

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RESULT 12
US-10-011-125-4
; Sequence 4, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804F1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 281
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-011-125-4

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RESULT 13
US-10-001-054-S4
; Sequence 54, Application US/10001054
; Publication No. US20020192209A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David

APPLICANT:	Smith, Victoria
APPLICANT:	Watanabe, Colin
APPLICANT:	Wood, William
TITLE OF INVENTION:	METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION:	CELL GROWTH
FILE REFERENCE:	P3034R1PCT
CURRENT APPLICATION NUMBER:	US/10/001,054
CURRENT FILING DATE:	2001-11-30
PRIOR APPLICATION NUMBER:	60/059114
PRIOR FILING DATE:	1997-09-17
PRIOR APPLICATION NUMBER:	60/079689
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079920
PRIOR FILING DATE:	1998-03-30
PRIOR APPLICATION NUMBER:	60/082999
PRIOR FILING DATE:	1998-04-24
PRIOR APPLICATION NUMBER:	60/083545
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/085149
PRIOR FILING DATE:	1998-05-12
PRIOR APPLICATION NUMBER:	60/087607
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PRIOR APPLICATION NUMBER:	60/088858
PRIOR FILING DATE:	1998-06-11
PRIOR APPLICATION NUMBER:	60/090691
PRIOR FILING DATE:	1998-06-25
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; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
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; PRIOR FILING DATE: 1999-10-18
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; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
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; PRIOR APPLICATION NUMBER: 09/866034
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; PRIOR APPLICATION NUMBER: 09/872035
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; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 2001-08-13
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; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
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; PRIOR APPLICATION NUMBER: PCT/US00/00376
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; PRIOR FILING DATE: 2000-02-18
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; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15

; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
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; PRIOR APPLICATION NUMBER: PCT/US00/22031
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; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
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; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match 100.0%; Score 1478; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MAMMEVGGPSLGTQCVLIIVFTVLLQSLCAVATYVYFTNELKQMDKYKSGIACFLKE	60
Qy	61	DDSYWDPNDEESMNSPCWQVKWLRLQVRKMLRTSEETISTYQEKQONISPLVRERGPO	120
Db	61	DDSYWDPNDEESMNSPCWQVKWLRLQVRKMLRTSEETISTYQEKQONISPLVRERGPO	120
Qy	121	RVAAHITGTGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG	180
Db	121	RVAAHITGTGRNTLSSPNKNEKALGRKINSWESSRSGHSLNHLNGLVTHEKG	180
Qy	181	FYIYSQTYPRFQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSNRSCWSDAEVGLY	240
Db	181	FYIYSQTYPRFQBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSNRSCWSDAEVGLY	240
Qy	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281
Db	241	SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG	281

RESULT 14

US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.

APPLICANT: Karpf, Adam R.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REFERENCE: PA-0047 US
CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 54
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
QY 61 DDSYWDNDDEESMNSPCWQVKQLRQVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
Db 61 DDSYWDNDDEESMNSPCWQVKQLRQVVRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

RESULT 15
US-10-174-654-11
Sequence 11, Application US/10174654
Publication No. US20030044937A1
GENERAL INFORMATION:
APPLICANT: Bienkowski, Michael J
Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11

Query Match 100.0%; Score 1478; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.8e-133;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MAMMEVGGPSLGGTCLVIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
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QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
Db 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVTHEKG 180
QY 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
Db 181 FYIYSQTYFRFOEEIKENTKNDKQWQVIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 281

Search completed: March 23, 2004, 09:12:35
Job time : 47 secs

R:Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
 A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
 A:Reference number: JC2340; MUID:95071350; PMID:7980502
 A:Accession: JC2340
 A:Molecule type: DNA
 A:Residues: 1-281 <MUT>
 A:Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PIDN:BAA07320.1; PID:g1369902
 R:Schatzlein, C.E.
 Submitted to the EMBL Data Library, June 1995
 A:Reference number: S57565
 A:Accession: S57565
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-281 <SCH>
 A:Cross-references: EMBL:X89102; NID:G887455; PID:G887456
 R:Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G.J. Exp. Med. 181, 71-77, 1995
 A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
 A:Reference number: I38554; MUID:95105731; PMID:7528780
 A:Accession: I38554
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-281 <RE2>
 A:Cross-references: EMBL:U08137; NID:G624627; PIDN:AAC50071.1; PID:G624628
 C:Genetics:
 A:Gene: FasL
 A:Introns: 151/1; 116/3
 C:Keywords: glycoprotein; transmembrane protein
 F:80-102/Domain: transmembrane #status predicted <TM>
 F:76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 186; DB 2; Length 281;
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 4 MEVGGPSLGTCLVIFVTLQSLCAV---TYVFTNELKQMDKYKSGIACFLKE 60
 71 LKRGHSTG-LCLLVFFVVALVGLGCMQLFHLKELAELESTQMTASLEK 129
 61 DSYWPDNDESMNSPCQVKQRLQRLVRKMLRTSEETISTVQEKQNTISPLVRBGPQ 120
 130 QIGHPSPPPE-----KXELRV----- 146
 121 RVAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSLNHLRNGELVIEHGK 180
 147 ---AHLT---GKNSRSM-----LEWPT-YGIVLLSGVKYKGLGVINETG 187
 181 FYIYSQTYRFOBEIKENTKNDKQVQIY-KYTSYPPDPILLMKGARN-----CWSK 233
 188 LFEVSKVYFRGQ-----SCNNLPLSHKVMNSKYPQDLVMEGKMWKSYCTTGQWVAR 241
 234 DAEGYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFGAP 278
 242 -----SSYLGAFAVNLTSADHLVYNVSELSLVNFESQTFGLY 279

RESULT 3
 A49266
 fas ligand - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: A49266
 R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
 Cell 75, 1169-1178, 1993
 A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
 A:Reference number: A49266; MUID:94084792; PMID:7505205
 A:Accession: A49266
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-278 <SD>
 A:Cross-references: GB:U003470; NID:G440178; PIDN:AAC52129.1; PID:G440179
 C:Keywords: glycoprotein; transmembrane protein

Query Match 12.0%; Score 177.5; DB 2; Length 278;
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 Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;
 100 ISTVQEKQONISPLVRERGPQVAAHITCT-RGRSNTLSSPNKNEKALGRKINSWESSR 158
 121 VSSFEQIANPSTPTKPRSV-AHLTGNPRSRISPL-----EWEDT- 162
 159 SGHSFLSNLHRNGELVIEHKGFIYISQTYRFOBEIKENTKNDKQVQIY-KYTSYP 217
 163 YGTALISGVKYYKGLVINEAGLYFYVSKYFRGQ-----SCNSQPLSHKVMNRNKYP 216
 218 DPILLMKSR-NSCWSKDAEYGLYSIQGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
 217 GDILVMEKKLVCTI--CQIWAHSSYLGAFAVNLTVADHLVYNISQSLINFEESKTFPG 274
 277 AF 278
 275 LY 276

RESULT 4
 S53090
 CD40 ligand - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
 C:Accession: S53090
 R:Wiertens, B.E.L.C.; Muriuki, M.
 submitted to the EMBL Data Library, February 1995
 A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
 A:Reference number: S53090
 A:Accession: S53090
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-261 <NER>
 A:Cross-references: EMBL:Z48469; NID:G732569; PIDN:CAA88363.1; PID:g732570

Query Match 11.1%; Score 164; DB 2; Length 261;
 Best Local Similarity 25.9%; Pred. No. 2.1e-06;
 Matches 72; Conservative 52; Mismatches 114; Indels 40; Gaps 14;
 6 VGGPSLGTCLVIFVTLVLL--QSLCAVAVTVYFTNELKQMDKYKSGIACFLKEDDS 63
 13 VATGPVSMK-IFMYLLTVFLITQIGSALFALVHLRLDKIEDERNLHEDFVFMK---T 68
 64 YWDPNDESMNS-PCQVKQRLQRLVRKMLRTSEETISTVQEKQNTISPLVRBGPOR 121
 69 IQRCNKGGESLJLNCCEIRSFEDLV-KDINQKE-----VKKKKNFEMHKGQDEPO- 121
 122 VAAHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSLN--LHLRNG-ELVIEH 178
 122 IAAHV-----ISEASSKTTSVL-----QW--APKGYVTLNNVLTLNGKQLAVKR 165
 179 KGFYIYSQTYRFOBEIKENTKNDKQVQIYKYTSYPPDPILLMKSRNSCWSKDAEYG 238
 166 QGFYIYITQVTPCSNRE---TLQAPFIASLCLSPSGSERILLRAANTHSSSKPC--G 219
 239 LYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
 220 QQSILHGGVFELOSGASVFNVTDPSSQVSHGTGFTSFG 257

RESULT 5
 I53476
 CD40 ligand - human
 N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
 C:Accession: S28017; JH0793; S26852; S2852; I53476; S25684; S30593
 R:Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
 EMBO J. 11, 4313-4321, 1992
 A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand fo

C:Accession: S21738
R:Amikage, R.J.; Fanslow, W.C.; Stockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff, B
P;Cosman, D.; Springs, M.K.
Nature 357, 80-82, 1992
A:Title: Molecular and biological characterization of a murine ligand for CD40.
A:Reference number: S21738; MUID:52244364; PMID:1374165
A:Accession: S21738
A:Molecule type: mRNA

RESULT 9

S12606
tumor necrosis factor alpha precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S12606; S17290; S18965; I46659
R:Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A:Title: Gene sequence of porcine tumor necrosis factor alpha.
A:Reference number: S12606; MUID:91016861; PMID:2216741
A:Accession: S12606
A:Molecule type: DNA
A:Residues: 1-232 <DBE>
A:Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
R:Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative ana
A:Reference number: S17289; MUID:91340150; PMID:1874444
A:Accession: S17290
A:Molecule type: DNA
A:Residues: 1-232 <KHU>
A:Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
A:Note: the authors translated the codon GAG for residue 202 as Gly
R:Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis f
A:Reference number: S18965
A:Accession: S18965
A:Molecule type: mRNA
A:Residues: 1-232 <CHO>
A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R:Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reactio
A:Reference number: I46659; MUID:90034181; PMID:2478420
A:Accession: I46659
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 44-232 <PAU>
A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C:Genetics:

```

A;Introns: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19_20/Binding site: myristate (lys) (covalent) #status predicted
F;81/Binding site: carboxydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

Query Match          9.0%; Score 133; DB 1; Length 232;
Best Local Similarity 21.3%; Pred. No. 0.00076;
Matches 61; Conservative 40; Mismatches 100; Indels 86; Gaps 11;

Qy  2  AMMEVOGSPSLGTCVLVLIFTVLLQSLCAVATVTVFTNELKQMDKYSGKIACFLKED 61
      | : | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db  16  ALAKAGGPOGSRCLCLSLFSFLL---VAGATTLEF-----CLLHFE 54

Qy  62  DSYWDPNDESMNSPCWQVKWQLRQLVRKMLRTSETISTVQEKQONISPLVRERGPQR 121
      | | | | | | | | | | | | | | | | | | | | | | : | : | :
Db  55  --VIGPQKEFPAGPL-----SINPLAQ----- 75

Qy  122  VAAHITGTRGRNTLSPNS---KNEKALGRKINSWESSRSGHSFSLNHLRNGELVIHE 178
      | | | | | | | | | | | | | | | | | | | | | | : | : | :
Db  76  -----GLRSSQTSDKPVAHVAVNKAEGQL--QMOSGVANALLANGVKLKNQVLVPT 127

Qy  179  KGFYIIYSQYFPFQBEIKEN---TKNDKQMVQVIYKYTSYDPDILLMKARSWSK-- 233
      | | | | | | | | | | | | | | | | | | | | | | : | : | :
Db  128  DGLYIIYSQVLFRRGQGCPSFNVLTHLTISRIA-----VSQTKVNLLLSAIKSPQRET 181

234  ---DAEVCIVSYVGGCTETPKNDKDEIVSYVNHITMDRPAQ-SEC 276

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QY 231 ---WSKDAEGLYSIVQGGIFELKENDRIFVSVTNHLLDMDHEAS-FPG 276
Db 181 TPEWA-EAKPWEPIYQGGVQLEKGRDLRAEINLFDYLAESGGVYFG 229

RESULT 13
154490
tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C:Accession: I54490
R:Crew, M.D.; Filipowski, M.E.
Immunogenetics 35, 351-353, 1992
A>Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus
A:Reference number: I54490; MUID:92218012; PMID:1348497
A:Accession: I54490
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C:Genetics:
A:Gene: PTNPF
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19/20/Binding site: myristate (lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 8.8%; Score 129.5; DB 2; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.0015;
Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

QY 110 ISPLVRRGQPVAAHITGRGSRNVL-SSPNSKNEKALGRKINSWE-----SSRSGH 161
Db 56 IGPQREEKFNPLP--IIGSMQTLTLRRSSQSSDKPVAHVAVNHQVDEQLWLSRGAN 113

QY 162 SFLSN-LHLRNGELVTHEKGFYIVSYQTFRFOEIKENTKDKQVQYIKY-TSYDPD 219
Db 114 ALLANGMOLKDNQIVLPADGLVLYVSQLFKGQ-----GCSSVLLTHVTRFAVSYEDK 168

QY 220 ILMKSGARNSCWGSKDAEYG-----LYSVYQGGIFELKENDRIFVSVTNHLLDMDHEAS 273
Db 169 VNLLSAISKSPC-KRETPEGSELKPWEPIYLGGVQLEKGRDLRAEINLFDYLAESGG 227

QY 274 -FPG 276
Db 228 VYFG 231

RESULT 14
S24641
lymphotoxin - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I46046; S24641
R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A>Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumor necrosis factor genes
A:Reference number: I46046; MUID:94083525; PMID:8260599
A:Accession: I46046
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <CL2>
A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
C:Genetics:
A:Introns: 32/3; 68/1
C:Superfamily: tumor necrosis factor

Query Match 8.6%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.0019;
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 99 TISTVQEKQNI SPLVRGQPVAAHITG-----TRGRSNTLSPNSKNEKALGRKI 151

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Db 40 TFSASQPAHQQL-PTFFTRGTLPAAHLVGPSTQDSLWRANT-----DRAFLR-- 88
QY 152 NSWSSRSRSHSFLSNLHRLNGELVTHEKGFYIVSYQTFRFOEIKENTKDKQVQYIKY 211
Db 89 -----HGF-----SLSNSLLVPTSLGLFVYVQVFGCGFPFRATPTPLYLAHEVQ 135
QY 212 KYT-SYDPDILLMKSGARNSCWGSKDAEYGLYSIVQGGIFELKENDRIFVSVTN-EHLIDMD 269
Db 136 LFSQPPHFVPLLSAQKSVCPGQPGPW-VRSYVQGAVALLLTRGDQLSTHTDGIHLL-LS 193
QY 270 HEASPFEGAF 278
Db 194 PSSVFFGAF 202

RESULT 15
OWHUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin, TNFA
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B2
R:Nedwin, G.E.; Navlor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica,
Nucleic Acids Res. 13, 6361-6373, 1985
A>Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr
A:Reference number: A93585; MUID:86016093; PMID:2995927
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <NED>
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
R:Tris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurek
Nature Genet. 3, 137-145, 1993
A>Title: Dense Alu clustering and a potential new member of the NF-kappaB family within
A:Reference number: S36153; MUID:93272029; PMID:8499947
A:Accession: S36153
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <IRI>
A:Cross-references: EMBL:215026; NID:g37211; PIDN:CAA78745.1; PID:g37212
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A>Title: Human tumour necrosis factor: precursor structure, expression and homology to
A:Reference number: A93351; MUID:85086244; PMID:6392892
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PEN>
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A>Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyel
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A>Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190; PMID:3856324
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', 64-233 <WAN>
A:Cross-references: GB:M10988; NID:g39373; PIDN:AAA61198.1; PID:g393738
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; A
Lymphokine Res. 7, 175-185, 1988
A>Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta ar
A:Reference number: A61478; MUID:88301617; PMID:2841543
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102;109-119;121-128, 'X',130-131;142-144, 'X',146, 'XXX',150-152;159-174;18
R:Marneout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A>Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A:Reference number: I53311; MUID:86030296; PMID:3932069
A:Accession: I53311
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <MAR>

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A;Cross-references: GB:H26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A;Experimental source: U-937 cells
R;Takakura-Yamamoto, K.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
A;Accession: S62610
A:Molecule type: protein
A;Residues: 77-99 <TAK>
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-8 <DAL>
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysines
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hase, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bringas
J. Biol. Chem. 269, 2345-2354, 1994
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:95130974; PMID:3871770
C;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
out detriment to normal cells. It can also act synergistically with interferon gamma to
C;Comment: TNP-alpha and -beta (lymphotoxin) are the products of different genes closely
related which are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:L20441; OMIM:191160
A;Map position: gp21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxicity; glycoprotein; homotrimer; lipoprotein; lymphokine; macropain
F;1-76/Domain: propeptide #status predicted <PRO>
E;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) [partial] #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match 8.5% Score 125.5; DB 1; Length 233;
Best Local Similarity 17.8%; Pred.No. 0.0033;
Matches 51; Conservative 52; Mismatches 99; Indels 85; Gaps 9;

Qy 2 AMMEVQGSGSLGTCVLIVITFTLLQLSCVAVTYVFYNELKQMOKDYKSIGACFLKEK 61
Db | : | : | : | : | : | : | : | : | : | : | : | : | :
 16 ALPKTKGGPGQSRRCLFLSFLIVAGATTLCPLLHFGVGIPQREFFR----- 65

Qy 62 DSYPDNDSEMSPCWVKWKLRLVRKMILTSSETISTVQEKQONTPLVRGPQR 121
Db | : | : | : | : | : | : | : | : | : | : | : | : | :
 66 -----DSLISPLAQ-----VASSRTPS-----DK 87

Qy 122 VAAHITGRSNTLSSPNSKNKALCRKINSVESRSGHSLNLHLNGELAVIHEKG 181
Db | : | : | : | : | : | : | : | : | : | : | : | : | :
 88 PVAHVIA-----NQAEQL---QMLNRANALLANGVELRDNLVVPSGL 131

Qy 182 YYYYSQTYFRFOEEIKENTNKDMQVQIIKYKT-----SYDPFILMKSRNSCSWK-- 233
Db | : | : | : | : | : | : | : | : | : | : | : | : | :
 132 YLIYSQVLFXQG-----GCPSTHVLTHTHSRIASVSQTKNVLSAIKSPCCQETP 182

Qy 234 ---DAEYGLSIYCQGIPELKENDIRFSVTVNEHLDMDHEAS-FPG 276
Db | : | : | : | : | : | : | : | : | : | : | : | : | :
 183 EGAEAPKWPIYLGVGFQEGKRDSAEINRPDIYDLDFAESGVGYFG 229

Search completed: March 23, 2004, 09:07:19
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:03 ; Search time 17 Seconds
(without alignments)

860.689 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVQGGPSLQGTCTLV.....NEHLIDMDHEASPFGLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	1	TN10 HUMAN
2	930	62.9	231	1	TN10 MOUSE
3	267.5	18.1	318	1	TN11 RAT
4	258.5	17.5	316	1	TN11 MOUSE
5	251.5	17.0	317	1	TN11 HUMAN
6	189.5	12.8	279	1	TN10 MOUSE
7	187	12.7	280	1	TN10 CERTO
8	185	12.6	281	1	TN10 HUMAN
9	185	12.5	280	1	TN10 MACMU
10	184	12.4	272	1	TN10 CHICK
11	182	12.3	282	1	TN10 PIG
12	177.5	12.0	278	1	TN10 RAT
13	164	11.1	261	1	TN10 BOVIN
14	160	10.8	174	1	TN10 HUMAN
15	159.5	10.8	240	1	TN10 HUMAN
16	152.5	10.3	239	1	TN10 MOUSE
17	152	10.3	261	1	TN10 CALJA
18	150.5	10.2	261	1	TN10 AOTTR
19	149.5	10.1	260	1	TN10 FELCA
20	148	10.0	261	1	TN10 MACMU
21	147.5	10.0	260	1	TN10 CANPA
22	147.5	10.0	261	1	TN10 HUMAN
23	143	9.7	261	1	TN10 PIG
24	140	9.5	260	1	TN10 MOUSE
25	136.5	9.2	235	1	TN10 RABIT
26	135	9.1	229	1	TN10 CEREL
27	134.5	9.1	204	1	TN10 PIG
28	134	9.1	234	1	TN10 BOSIN
29	133.5	9.0	260	1	TN10 RAT
30	133	9.0	232	1	TN10 PIG
31	133	9.0	234	1	TN10 CAVPO
32	131.5	8.9	233	1	TN10 BUBBU
33	131.5	8.9	233	1	TN10 PAPSP

RESULT 1

ID	TN10 HUMAN	STANDARD	PRT	281 AA
AC	P50531			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).			
GN	TNFSF10 OR TRAIL OR APO2L			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96111955; PubMed=8777713;			
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nichol J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF family that induces apoptosis."			
RL	Immunity 3:673-682(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96278649; PubMed=86631110;			
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A., Ashkenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."			
RL	J. Biol. Chem. 271:12687-12690(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
RX	MEDLINE=23388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Maman A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

ALIGNMENTS

34	131	8.9	234	1	TNFA HORSE	P29553	equus caball
35	131	8.9	253	1	TNFA SPAAU	Q81fg3	sparus aura
36	130.5	8.8	233	1	TNFA BOVIN	Q06599	bos taurus
37	129.5	8.8	235	1	TNFA PERLE	P36939	peromyscus
38	127.5	8.6	204	1	TNFB BOVIN	Q06600	bos taurus
39	127.5	8.6	233	1	TNFA MARMO	P35734	marwortia mon
40	125.5	8.5	233	1	TNFA HUMAN	P01375	homo sapien
41	123.5	8.4	235	1	TNFA MOUSE	P06804	mus musculu
42	123.5	8.4	235	1	TNFA RAT	P16599	rattus norv
43	122	8.3	205	1	TNFB HUMAN	P01374	homo sapien
44	122	8.3	232	1	TNFA PANTR	Q8hzd9	pant troglod
45	122	8.3	234	1	TNFA CAPHI	P32996	castra hircu

P29553	equus cabal
O8jfg3	sparus aura
Q06599	bos taurus
P36939	peromyscus
Q06600	bos taurus
O35734	marmota mon
P01375	homo sapien
P06804	mus musculus
P16599	rattus norv
P01374	homo sapien
Q8hd99	pan troglod
P13296	capra hircu

[4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE=20017054; PubMed=10549288;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RT complex with death receptor 5";
 RL Mol. Cell 4:563-571(1999).
 [5]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RP PubMed=10542098;
 RX Mongkoleapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Sreaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 [6]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RP MEDLINE=99413670; PubMed=10485660;
 RX Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 RT selective antitumor activity";
 RL Immunity 11:253-261(1999).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1.
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -I- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -I- SUBUNIT: Homotrimer.
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -I- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 CC AND PROSTATE.
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U37518; AAC50332.1; -;
 DR EMBL; U57059; AAB01233.1; -;
 DR EMBL; BC032722; AAH32722.1; -;
 DR PDB; 1D0G; 22-OCT-99.
 DR PDB; 1D4V; 01-NOV-99.
 DR PDB; 1D2Q; 11-FEB-00.
 DR PDB; 1D6G; 26-SEP-01.
 DR GENE; HGNC:11925; TNFRSF10.
 DR MIM; 603598; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0005625; C: soluble fraction; TAS.
 DR GO; GO:0005102; F: receptor binding; TAS.
 DR GO; GO:0007267; P: cell-cell signaling; TAS.
 DR GO; GO:0006917; P: induction of apoptosis; TAS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00251; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 KW Zinc; 3D-structure.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 39 281 (POTENTIAL).
 FT METAL 230 230 EXTRACELLULAR (POTENTIAL).
 FT STRAND 123 127 ZINC.
 FT TURN 130 131
 FT TURN 137 139
 FT STRAND 149 150
 FT STRAND 163 165
 FT STRAND 167 170
 FT TURN 171 172
 FT STRAND 173 176
 FT STRAND 180 193
 FT STRAND 205 213
 FT STRAND 220 228
 FT STRAND 237 250
 FT TURN 252 253
 FT STRAND 255 260
 FT HELIX 263 265
 FT STRAND 266 267
 FT TURN 270 272
 FT STRAND 274 281
 SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;
 Query Match 100.0%; Score 1478; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred No. 8e-115;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMVEQGQPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 DB 1 MAMVEQGQPSLGQTCVLIVFTVLQSLCAVAVYVFTNELKQMDKYSGIACFLKE 60
 QY 61 DSYWDPNDEESNPGCWQKQLVVKMLRTSEETISTVQEQQNISPLVRRGPQ 120
 DB 61 DSYWDPNDEESNPGCWQKQLVVKMLRTSEETISTVQEQQNISPLVRRGPQ 120
 QY 121 RYAAHTTGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKG 180
 DB 121 RYAAHTTGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKG 180
 QY 181 FYYISQTYFRQEEIKENTKNDKQVQYIYKYTSPDPILLMKSGNSKDAEYGLY 240
 DB 181 FYYISQTYFRQEEIKENTKNDKQVQYIYKYTSPDPILLMKSGNSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 2
 TN10_MOUSE
 ID TN10_MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT Identification and characterization of a new member of the TNF
 RT family that induces apoptosis";
 RL Immunity 3:673-682(1995).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

Query Match 18.1%; Score 267.5; DB 1; Length 318;
 Best Local Similarity 27.3%; Pred. No. 8e-15;
 Matches 82; Conservative 55; Mismatches 106; Indels 57; Gaps 11;

QY 10 PSIGQTCVLIVFTVLQSLCAVAVTVYFTELKQMDQKYSKGIACF-----LKED--- 61
 DB 43 PAASRFMFALGLGLGQGVVCSIALFLYFRAQMD--PNRISEDSSTCFYRIILRENTGL 100
 QY 62 -DSYNDPNDDEESMNSPCWQVKWQLRQLVKRMILRTSEETISTVQEQKQNISPLVRGRGP 120
 DB 101 QDSTLESEDEALPDCSRMKQAFQ-----GAVQRELOHIV-----GQ 139
 QY 121 R---VAAHITGT-----RGRS-----NTLSPNSKNEKALGRKINWESRSRH 161
 DB 140 RFGSGVPAMEGSLDVARRGKPEAQPFAHLTINAADIPSGSHKVSF-----SSWYHDR-GW 194
 QY 162 SFLSNLHLRNGELVIEHKEGFIYIYSQTYRFRQFEIKENTKNDKQWQYIYKYT-SYDPDI 220
 DB 195 AKISNLTSLNGKLRVNDQGFYIYANICPRHETSGSVPADYVQLMVMYVVKTSIKIPSSH 254
 QY 221 LLKMSARNCSWGDARFYGLYSYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFLV 280
 DB 255 NLKMGSGTKNSGNSBFHYFSINVGFFFKLRAGEEISVQVNSPLSLDPDQATYFGAFKV 314

RESULT 4

TN11 MOUSE STANDARD; PRT; 316 AA.

ID TN11 MOUSE AC Q35235; Q35306; Q9JUK8; Q9JUK9; Q9R1Y0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
 DE (OCIF)
 GN TNFRSF11 OR RANKL OR TRANCE OR OPGL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hybridoma; PubMed=93121212;
 RX MEDLINE=97460112; PubMed=93121212;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
 RT that activates c-Jun N-terminal kinase in T cells.";
 RL J. Biol. Chem. 272:25190-25194(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=98032977; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tomesko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow;
 RX MEDLINE=98227661; PubMed=9568710;
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
 RA Burgess J., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
 RA Sullivan T., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
 RA Boyle W.J.;
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast

RT differentiation and activation.";
 RL Cell 93:165-176(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow stroma;
 RX MEDLINE=98188248; PubMed=9520411;
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
 RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
 RT "Osteoclast differentiation factor is a ligand for
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
 RT to TRANCE/RANKL.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129;
 RX MEDLINE=99214075; PubMed=10196481;
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
 RA Ueda M., Higashio K.;
 RT "Cloning and characterization of the gene encoding mouse osteoclast
 RT differentiation factor.";
 RL Gene 230:121-127(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21150053; PubMed=11250921;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of three isoforms of the receptor activator of nuclear
 RT factor-kappaB ligand and their differential expression in bone and
 RT thymus.";
 RL Endocrinology 142:1419-1426(2001).
 RN [7]
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
 RX MEDLINE=99240759; PubMed=10224132;
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
 RT "Evidence for a role of a tumor necrosis factor-alpha
 RT (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a
 RT TNF family member involved in osteoclastogenesis and dendritic cell
 RT survival.";
 RL J. Biol. Chem. 274:13613-13618(1999).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
 RX MEDLINE=21464816; PubMed=11581298;
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
 RT of receptor-ligand specificity.";
 RL J. Clin. Invest. 108:971-979(2001).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
 RX MEDLINE=21839021; PubMed=11733492;
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at
 RT 2.2-A resolution.";
 RL J. Biol. Chem. 277:6631-6636(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O35235-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35235-2; Sequence=VSP_006449;
 CC Name=3;
 CC IsoId=O35235-3; Sequence=VSP_006448;

[3] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RP Ikeda T., Kuroyama H., Hirokawa K.;
RA "Determination of human RANKL isoforms";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE OF 73-317 FROM N.A.
RC TISSUE=Thymocytes;
RX MEDLINE=97460112; PubMed=93121132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlicki J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RL that activates c-Jun N-terminal kinase in T cells.";
RN J. Biol. Chem. 272:25190-25194(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Tongue;
RX MEDLINE=20175237; PubMed=10708588;
RA Nagai M., Kyakumoto S., Sato N.;
RT "Cancer cells responsible for humoral hypercalcemia express mRNA
RT encoding a secreted form of ODF/TRANCE that induces osteoclast
RL formation.";
RC Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
CC Secreted (isoform 2). A soluble form of isoform 1 arises by
CC proteolytic processing (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=O14788-1; Sequence=Displayed;
CC Name=2; Synonyms=SODF;
CC IsoId=O14788-2; Sequence=VSP_006447;
CC Name=3;
CC IsoId=O14788-3; Sequence=VSP_006446;
CC -!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK
CC IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC -!- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing (By similarity). The cleavage may be
CC catalyzed by ADAM17.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC EMBL; AF019047; AAC86811.1; -
CC EMBL; AF053712; AAC39731.1; -
CC EMBL; AB064269; BAB79694.1; -
CC EMBL; AB061227; BAB71768.1; -
CC EMBL; AB064270; BAB79695.1; -
CC EMBL; AF013171; AAC51762.1; -
CC EMBL; AB037599; BAA90488.1; -
CC HSSP; P50591; ID0G.
CC Genew; HGNC:11926; TNFSF11.
CC MIM; 602842; -
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0005887; C:integral to plasma membrane; NAS.

DR GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0030316; P:osteoclast differentiation; NAS.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; FALSE_NEG.
DR PROSITE; PS0049; TNF 2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor; Alternative splicing.
FT CHAIN 1 317
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 11, MEMBRANE FORM.
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT CLEAVAGE (BY SIMILARITY).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT Missing (in isoform 3).
FT /FTID=VSP_006446.
FT VARSPLIC 1 47
FT VARSPLIC 1 73
FT Missing (in isoform 2).
FT /FTID=VSP_006447.
FT CONFLICT 194 194 A -> G (IN REF. 4).
FT SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;
SQ
Query Match 17.0%; Score 251.5; DB 1; Length 317;
Best Local Similarity 24.1%; Pred. No. 1.7e-13;
Matches 71; Conservative 61; Mismatches 11; Indels 45; Gaps 10;
QY 10 PSLGTCVLIVFTVLLQSLCVAVTVYFTTNELKQMDKYSKSIACF-----LKED--- 61
DB 42 PAASRSMFVALLGLGQVVCVSVALFFYFRAQMD--PNRISDGTGTCIVRLILHENADF 99
QY 62 -DSYWDPNDEESMNSPCWQVKM-----QRLQVLRKMLRTSEETI-----STVQEKQ 107
DB 100 QDTTLESQDTKLIPDCRRIKQAFQAVQKELQHVGSQHRAEKAMVDGSLDLAKRSK 159
QY 108 QNISPLVREGRQVAAHITGTRGSNTLSSPNSKNEKALGRKINSMESSRSHSFLSNL 167
DB 160 LEAQPF-----AHUT-----INATDIPSGSHKVS-----SSWYHDR-GWAKISNM 199
QY 168 HLRNGELVIHEKGFYIYSQTYFRPQEEIKENTKNDKQMVQVIYKYT-SYDPILLMKSA 226
DB 200 TFSNGKLIWQDGFYLYLVANICFRHETSGDLATEYLQLMVTVTKTSIKIPSSHTLMKG 259
QY 227 RNSCWSKABYGLYIYQGGIFELKENDRIFVSVTHLIDMDHEASFGAFIV 280
DB 260 STKYWSGNSEPHFYSINVGGFFKLRSGEEISTEVSNPSLLDDPDQATYFGAPKV 313
RESULT 6
TNF6_MOUSE
ID TNF6_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).
DE GN TNFSF6 OR FASL OR APTL1 OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;

RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=BALB/c;
RA Fennel M.H., Shioda T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=C3H; TISSUE=Spleen;
RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: A new alternatively
RT spliced product of the mouse Fas ligand gene.";
RL Blood 94:3456-3467(1999).
RN [6]
RP CHARACTERIZATION OF VARIANT GLD.
RX MEDLINE=96091792; PubMed=7495745;
RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,
RA Rausseau M., Bron C., Renno T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice.";
RL Int. Immunol. 7:1381-1386(1995).
RN [7]
RP VARIANTS ALA-184 AND GLY-218.
RX STRAIN=C57BL/6, C3H, MRL, SJL, NOD, NZB, NZW, BALB/c, DBA/1, and
RA DBA/2;
RX MEDLINE=97268671; PubMed=9108079;
RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
RA Yagita H.;
RT "Polymorphism of murine Fas ligand that affects the biological
RT activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects (By similarity).
CC -1- SUBUNIT: Homotrimer (Probable).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
CC Secreted (isoforms FASL and FASLS).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=FasL;
CC IsoId=P41047-1; Sequence=Displayed;
CC Name=FasLS;
CC IsoId=P41047-2; Sequence=VSP_006445;
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- DISEASE: A deficiency in this protein is the cause of generalized

CC lymphoproliferation disease phenotype (gld). Gld mice present
CC lymphadenopathy and autoantibody production. The phenotype is
CC recessively inherited.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC -----
CC EMBL: U06948; AAA17800.1; -
CC EMBL: U10984; AAA19778.1; -
CC EMBL: S76752; AAB33780.1; -
CC EMBL: U58985; AAB02915.1; -
CC EMBL: AF119335; AAD52106.1; -
CC FIR: A53062; A53062.
CC HSSP: P01375; 4TSV.
CC MGD: MGI:99255; Tnfsf6.
CC InterPro: IPR008064; Fas ligand.
CC InterPro: IPR006053; TNF_abc
CC InterPro: IPR006052; TNF_family.
CC InterPro: IPR008983; TNF_like.
CC InterPro: IPR003636; TNF_subf.
CC Pfam: PF00229; TNF; 1.
CC PRINTS: PR01681; FASLIGAND.
CC PROSITE: PR01234; TNCRSISFCT.
CC ProDom: PD002012; TNF_subf; 1.
CC SMART: SM00207; TNF; 1.
CC PROSITE: PS00251; TNF 1; 1.
CC PROSITE: PS0049; TNF 2; 1.
CC KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
CC Disease mutation; Polymorphism; Alternative splicing;
CC FT CHAIN 1 279 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT MEMBER 6, MEMBRANE FORM.
CC FT CHAIN 128 279 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 4 69 PRO-RICH.
CC FT DOMAIN 45 51 POLY-PRO.
CC FT SITE 127 128 CLEAVAGE (BY SIMILARITY).
CC FT DISULFID 200 231 POTENTIAL.
CC FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPLIC 1 210 Missing (in isoform FASLS).
CC FT /FTid=VSP_006445.
CC FT VARIANT 184 184 T -> A (IN STRAINS BALB/C AND DBA;
CC FT ENHANCES CYTOTOXICITY).
CC FT VARIANT 218 218 E -> G (IN STRAINS BALB/C AND DBA;
CC FT ENHANCES CYTOTOXICITY).
CC FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL
CC FT TO ITS RECEPTOR).
CC SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;
CC
CC Query Match 12.8%; Score 189.5; DB 1; Length 279;
CC Best Local Similarity 25.8%; Pred. No. 1.9e-08;
CC Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;
CC
CC QY 83 QLRQLVRKMLTSETISTVQEKQNTISPLVRGQPVAAHITGRSNTLSPNSK 142
CC Db 111 ELREFTNQSL-----KVSSFEKQIANPSTPSEKPRSV-AHLTG-----NPHSR 154
CC QY 143 NKKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTQN 202
CC Db 155 SIPL-----EWEDT-YGTALISGVKYGKGLVINETGLYFYVSKYVFGQ-----SCN 201

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QY 203 DKOMQVYIY-KYTSYDPDILLMKSAR-NSCWSKDAEYGLYSIYGGIFELKENDRIFFSV 260
Db 202 NQPLNKHVNRNSKYEDLVIMBEKRLNYCTT--GQIWAHSYLGAVNLTSDSHLYVNI 259

QY 261 TNEHLIDMDHEASFFGAF 278
Db 260 SQLSLINFESKTFGLY 277

RESULT 7
TNF6 CERTO
ID TNF6 CERTO STANDARD; PRT; 280 AA.
AC Q9BDN1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RL Fas/FasL ligand and co-stimulatory molecules.";
CC Immunogenetics 53:315-328(2001).
CC -!- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects (By similarity).
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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or send an email to license@isb-sib.ch).

-----
DR EMBL; AF348487; AAK37606.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRODOM; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF; 1.
DR PROSITE; PS00049; TNF; 2; 1.
KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY.
FT MEMBER 6, MEMBRANE FORM.
FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY.

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FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT TRANSMEM 81 101 CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT EXTRACELLULAR (POTENTIAL).
FT PRO-RICH.
FT POLY-PRO.
FT CLEAVAGE (BY SIMILARITY).
FT SITE 128 129 POTENTIAL.
FT DISULFID 201 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 12.7%; Score 187; DB 1; Length 280;
Best Local Similarity 22.1%; Pred. No. 3e-08;
Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;

QY 4 MEVQGPSLGQTCVLIVITVLLQSLCVAVTVVYFTNELKOMQDKYSKGIACELKEDDS 63
Db 70 LKRGHSTG-ICLLVFMFVNLVALVGLGFMQLFLOKELAE-----LRETS 118
QY 64 YWDPNDEESMSPQWQVQWQLRQLVRKMLRTSEETISTVQEKQKNISPLVRERGQVVA 123
Db 119 -----QKHTASSLEKQIGHPS-PPEKKEQKV 145
QY 124 AHITGRGRSVTLSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEKGFY 183
Db 146 AHLTG-----KPNRSRMP-----EWEDT-YGIVLLSGVYKKGGLVINETGLYF 189
QY 184 IYQTVRFOEBIKENTKNDKQVQYIY-KYTSYDPDILLMKSARNCSKDAEYGLYSI 242
Db 190 VISKYVFRQ-----SCNLPFSHKVYMRNSKYQDVLVMEGRKMS-YCTTGQMWAHSS 242
QY 243 YQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAF 278
Db 243 YLGAVENLTSTDHLYVNVSELSLVNFERSQTFGLY 278

RESULT 8
TNF6 HUMAN STANDARD; PRT; 281 AA.
AC P48023; Q9BZP9;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN TNFSF6 OR FASL OR APTL1G1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RL lymphocytes.";
RN [2]
RX SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
RL specificity.";
RN [3]
RX Int. Immunol. 6:1567-1574(1994).
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Schaeuble C.E., Poehmann R., Philippse P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).

```

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RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayaishi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RT Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
RT human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RA Wilkinson J.;
RN Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RN SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RN CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228058;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Sauteri P.,
RA Terakih A., Peitsch M.C., Tschopp J.;
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RN J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RN PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RN Nat. Med. 4:31-36(1998).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects.
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC into the extracellular fluid, probably by cleavage from the cell
CC surface.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;

```

```

CC CC IsoId=P48023-1; Sequence=Displayed;
CC CC Name=2;
CC CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
CC CC -!- PTM: N-glycosylated.
CC CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC CC -!- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
CC Lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
CC involving hemolytic anemia and thrombocytopenia with massive
CC lymphadenopathy and splenomegaly.
CC CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
CC CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674.g.htm".
CC CC
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CC CC
CC EMBL; X89102; CAA61474.1; -
CC EMBL; U08137; AAC50071.1; -
CC EMBL; U11821; AAC50124.1; -
CC EMBL; D38122; BAA07320.1; -
CC EMBL; AF288573; AAG60017.1; -
CC EMBL; Z96050; CAB09424.1; -
CC EMBL; BC017502; AAH17502.1; -
CC EMBL; AB013303; BAA32542.1; -
CC PIR; I38707; I38707.
CC HSSP; P01375; 1TNEF.
CC Genew; HGNC:11936; TNFSF6.
CC MIM; 134638; -
CC MIM; 601859; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005102; F: receptor binding; TAS.
CC GO; GO:0007267; P: cell-cell signaling; TAS.
CC GO; GO:0006917; P: induction of apoptosis; TAS.
CC GO; GO:0007155; P: signal transduction; TAS.
CC InterPro; IPR008064; Fas_ligand.
CC InterPro; IPR006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01581; FASLIGAND.
CC PRINTS; PR01234; TNFCROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS00049; TNF_2; 1.
CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
CC Alternative splicing; Antigen.
CC CHAIN 1 281
CC CHAIN 130 281
CC CHAIN 1 80
CC CHAIN 81 102
CC DOMAIN 103 281
CC DOMAIN 4 70
CC DOMAIN 45 65
CC SITE 129 130
CC DISULFID 202 233
CC CARBOHYD 184 184
CC CARBOHYD 250 250
CC CARBOHYD 260 260
CC VARSPIC 117 127
CC FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT FT MEMBER 6, MEMBRANE FORM.
CC FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT FT MEMBER 6, SOLUBLE FORM.
CC FT FT CYTOPLASMIC (POTENTIAL)
CC FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT FT (POTENTIAL).
CC FT FT EXTRACELLULAR (POTENTIAL).
CC FT FT PRO-RICH.
CC FT FT POLY-PRO.
CC FT FT CLEAVAGE.
CC FT FT POTENTIAL.
CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT FT STSQMHTASSL -> ATPVHPLKRS (in isoform
CC FT FT 2)
CC FT FT /FTId=VSP_006443.

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```
CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SURCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
DR EMBL; AF344856; AAK37539.1; -
DR EMBL; AB035138; BAA90294.1; -
DR EMBL; AB035139; BAA90295.1; -
DR EMBL; AB035140; BAA90296.1; -
DR HSP; P01375; 4TSV.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS00049; TNF 2; 1.
KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT FT CHAIN 1 280
FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT FT MEMBER 6, MEMBRANE FORM.
FT FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT FT CYTOPLASMIC (POTENTIAL).
FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT PRO-RICH.
FT FT POLY-PRO.
FT FT CLEAVAGE (BY SIMILARITY).
FT FT POTENTIAL.
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT S -> P (IN REF. 1).
FT FT SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;
FT SQ Query Match 12.5%; Score 185; DB 1; Length 280;
FT Best Local Similarity 22.1%; Pred. No. 4.4e-08;
FT Matches 61; Conservative 56; Mismatches 91; Indels 68; Gaps 10;
QY 4 MEVQGSPSLGQTCLVIPTVLLOSLCVATYYVFNTNELKQMODYKSKSGIACFLKEDDS 63
DB 70 LKKRGHNSTG-LCLLMFMFWMLVALVGLGLGMFQLPHLOKELAE-----LKSTS 118
QY 64 YWDPNDEESMNSPCQVKWLRLQRKMLRTSEETISTVQEKQNISPLVRERGQRVA 123
DB 119 -----OKHTASLEKIQIHPS-PPEKEQRKV 145
QY 124 AHITTRGRSNLTSSPNKNEKALGRKINSWSRSRSHGSFLSNLHLRNGELVTHEKGFFY 183
DB 146 ASLTG-----KPNSRSMPL-----EWEDT-YGVILLSGVKYKGGVLINETGLFY 189
QY 184 IYSQTYFRFOEIKENTKNDKMQVYI-KYTSYDDPILLMKSRNSCWSDAAYGLYSI 242
DB 190 VYSKYVFRGQ-----SCTNLFSLHKVMRNRSKYPQDLVMMERGRMS-YCTTGOMWAHS 242
QY 243 YOGGIFELKENDIRFVSVTNEHLIDMDHEASFAG 278
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Db      243 YLGAVERNLSADHLYNVNSELVLNFEESQTFGLY 278
RESULT 10
TNF5_CHICK
ID      TNF5_CHICK  STANDARD;      PRT;      272 AA.
AC      Q91B08;
DT      28-FEB-2003 (Rel. 41, Created)
DT      15-MAR-2004 (Rel. 43, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
GN      L) (CD154 protein).
DE      TNF5 OR CD40LG OR CD40L.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=White leghorn; TISSUE=Spleen;
RA      Tregaskes C.A., Young J.R., Burnside J.;
RL      "Cloning of a putative chicken CD40 ligand.";
RL      Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC      proliferation in the absence of co-stimulus as well as IGE
CC      production in the presence of IL-4. Involved in immunoglobulin
CC      class switching (By similarity).
CC      -!- SUBUNIT: Homotrimer (By similarity).
CC      -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC      extracellular soluble form (By similarity).
CC      -!- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AJ243435; CAB95748.2; --
CC      HSSP; P29965; ITALY
DR      GO; GO:0016021; C:integral to membrane; ISS.
DR      GO; GO:0005174; F:CD40 receptor binding; ISS.
DR      GO; GO:0042100; P:B-cell proliferation; ISS.
DR      GO; GO:0006954; P:inflammatory response; ISS.
DR      GO; GO:0007159; P:leukocyte cell adhesion; ISS.
DR      GO; GO:0030168; P:platelet activation; ISS.
DR      InterPro; IPR003263; TNF_5.
DR      InterPro; IPR006052; TNF family.
DR      InterPro; IPR008983; TNF like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      PRINTS; PR01702; CD40LIGAND.
DR      ProDom; PD008600; TNF_5; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF 1; 1.
DR      PROSITE; PS00049; TNF 2; 1.
KW      Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT      CHAIN          1 272
FT      CHAIN          111
FT      CHAIN          272
FT      DOMAIN          1 23
FT      TRANSMEM          24 44
FT      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT      (POTENTIAL).
FT      DOMAIN          45 272
FT      SITE            110 111
FT      CLEAVAGE (BY SIMILARITY).
FT      DISULFID          190 229

```

Query Match 12.4%; Score 184; DB 1; Length 272;
Best Local Similarity 25.4%; Pred. No. 5.1e-08;
Matches 69; Conservative 48; Mismatches 119; Indels 36; Gaps 9;

FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;

QY 16 CVLIIVFTVLLQSLCVAVTVYVFTNELKQMDQKYSKSGIACFLKEDDSYWDNDRESMNS 75
Db 26 CFLSFMVV--QTIGTVLFCFLYHMKMDKWEVLSDNEYIIFRKVKQCTQEDQKSTLL 83
QY 76 PCMQVQKQLRQLVRKMLFTSEETISTVOEKQONISPLVRERG-----QRVAAHIT 127
Db 84 DCEKVLKGFQDLQCKD--RTASEELPKFEMHGRGHEPHLKSNETSVAEKKEQPIATHLA 141
QY 128 GTRGSRNTLSSPNSKNEKALGRKINSW-ESSRSGHSFSLNHLRNGELVIHEKGFYIYS 186
Db 142 GV--KSNTTV-----RVLKMMTTSYAPTSSLSISYH--EGKLKVEKAGLYIYS 185
QY 187 QTYFRFQBEIKENTKNDKQMVQYIYKYTSYPDPPIILMKSRNSCWSKDAEYGLYSYIOGG 246
Db 186 QVSF-----CTKAAASAPFTLYIYLYPMEEDRLIMKGLDTHST--TALCELSIREGG 238
QY 247 IPELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Db 239 VPELRQGMVFVNVTSTAVNVNPGNTYFGMF 270

RESULT 11
TNF6_PIG
ID TNF6_PIG STANDARD; PRT; 282 AA.
AC Q9BEA8; Q95M04; Q95N10;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
GN ligand).
DE TNF6 OR FASL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21322533; PubMed=11429161;
RA Muneta Y., Shimoi Y., Inumaru S., Mori Y.;
RT "Molecular cloning, characterization, and expression of porcine Fas
RT ligand (CD95 ligand).";
RL J. Interferon Cytokine Res. 21:305-312(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Guanxi bama miniature pig;
RA Zhu N., Young Y.;
RT "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Tsuyuki S., Kono M., Bloom E.T.;
RT "Cloning and potential utility of porcine Fas ligand: overexpression
RT in porcine cells protects them from attack by human cytolytic cells.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;
RX MEDLINE=21653191; PubMed=11792426;
RA Moteji-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison
RT with human gene.";
RL Mol. Immunol. 38:581-586(2002).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RX MEDLINE=99091541; PubMed=9872942;
 RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
 RA Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
 RA Li L.-Y., Gentz R., Yu G.-L.;
 RT "VEGF1, a novel cytokine of the tumor necrosis factor family, is an
 RT angiogenesis inhibitor that suppresses the growth of colon carcinomas
 RT in vivo";
 RL FASEB J. 13:181-189(1999).
 CC -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
 CC (in vitro).
 CC -!- SUBUNIT: Homotrimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
 CC Detected in placenta, lung, kidney, skeletal muscle, pancreas,
 CC spleen, prostate, small intestine and colon.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 DR EMBL; AF039390; AAD08783.1; -;
 DR HSP; P50591; IDOG.
 DR Genew; HGNC:11931; TNFSF15.
 DR MIM; 604052; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0005102; F: receptor binding; TAS.
 DR GO; GO:000074; P: regulation of cell cycle; TAS.
 DR InterPro; IPR006053; TNF_family.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR008983; TNF_like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PSS0049; TNF; 2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; signal-anchor.
 FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 85 125 POTENTIAL.
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;
 Query Match 10.8%; Score 160; DB 1; Length 174;
 Best Local Similarity 35.3%; Pred. No. 2.7e-08;
 Matches 49; Conservative 24; Mismatches 46; Indels 18; Gaps 8;
 QY 154 WESSRSGHSLN-LHLRNGELVTHKGFYVYQTVFRFQ-----ERIKENTKDK--QM 206
 DB 42 WE-HELGLAFTKRMVYNTKELLIPESGDYFIYQVTFRGMTSECSIRAGRNKEDSI 100
 QY 207 VQYIKYKT-SYPDPILMKSRNSCSKDAFYG---LYSYQGQIFELKENDRIFVSVTN 262
 DB 101 TWVITKVTDSYPTQLLMGKTSVC-----EVGSNWQPIYLGAMFSLQSGDKLMVNVSD 155
 QY 263 EHLIDMDHE-ASFGFAIV 280
 DB 156 ISLDVYTKEDKTFGFAELL 174

RESULT 15
 TN14 HUMAN
 ID TN14 HUMAN STANDARD; PRT; 240 AA.
 AC Q43557; O75476; Q8WVF8; Q96LD2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
 DE mediator-ligand) (HVEM-L).
 GN TNFSF14 OR LIGHT OR HVEM-L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=98122340; PubMed=9462508;
 RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
 RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
 RA Ware C.F.;
 RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
 RT ligands for herpesvirus entry mediator";
 RL Immunity 8:21-30(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Liver;
 RX MEDLINE=98438532; PubMed=9765287;
 RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
 RA Tan K.B., Dede K., Spampinato J., Silverman C., Hensley P.,
 RA DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
 RA Truneh A., Young P.R.;
 RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
 RT HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
 RT growth";
 RL J. Biol. Chem. 273:27548-27556(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
 RX MEDLINE=21528948; PubMed=11673523;
 RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
 RT "Genomic characterization of LIGHT reveals linkage to an immune
 RT response locus on chromosome 19p13.3 and distinct isoforms generated
 RT by alternate splicing or proteolysis";
 RL J. Immunol. 167:5122-5128(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Cytokine that binds to TNFSF3/LTBR. Binding to the
 CC decoy receptor TNFSF6B modulates its effects. Activates NFkB,
 CC stimulates the proliferation of T cells, and inhibits growth of
 CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex

CC virus.
CC -|- SUBUNIT: Homotrimer.
CC -|- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoform 1); Cytoplasmic (isoform 2).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43557-1; Sequence=Displayed;
CC Name=2; Synonyms=LIGHT delta-TM;
CC IsoId=O43557-2; Sequence=VSP_006452;
CC TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
CC NONHEMATOPOIETIC TUMOR LINES.
CC -|- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
CC -|- PTM: N-glycosylated.
CC -|- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing.
CC -|- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -|- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 178.
CC -----
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CC -----
CC DR EMBL; AF036581; AAC39563.1; -
CC DR EMBL; AF064090; AAC25169.1; -
CC DR EMBL; AY028261; AAK26160.1; -
CC DR EMBL; BC018058; AAK18058.1; ALT_FRAME.
CC DR HSSP; P01375; 4TSV.
CC DR Genew; HGNC:11930; TNFSF14.
CC DR MIM; 604520; -
CC DR GO; GO:0005102; F:receptor binding; TAS.
CC DR GO; GO:0006917; P:induction of apoptosis; TAS.
CC DR GO; GO:0007165; P:signal transduction; TAS.
CC DR InterPro; IPR006053; TNF abc.
CC DR InterPro; IPR006052; TNF family.
CC DR InterPro; IPR008983; TNF like.
CC DR Pfam; PF00229; TNF; 1
CC DR PRINTS; PR01234; TNFCROSIPT.
CC DR ProDom; PD002012; TNF_subf; 1.
CC DR SMART; SM00207; TNF; 1.
CC DR PROSITE; PS00251; TNF 1; FALSE_NEG.
CC DR PROSITE; PS00049; TNF 2; 1.
CC KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
CC Alternative splicing.
CC CHAIN 1 240
CC FT CHAIN ?83 240 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT CHAIN MEMBER 14, MEMBRANE FORM.
CC FT DOMAIN 1 37 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
CC FT TRANSMEM 38 58 MEMBER 14, SOLUBLE FORM.
CC FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT (POTENTIAL).
CC FT DOMAIN 59 240 EXTRACELLULAR (POTENTIAL).
CC FT SITE 82 83 CLEAVAGE (POTENTIAL).
CC FT DISULFID 154 187 POTENTIAL.
CC FT CARBOHYD 102 102 N-LINKED (GLCNAC...).
CC FT VARSPLIC 38 73 Missing (in isoform 2).
CC FT CONFLICT 120 120 /FTIG=VSP_006452.
CC FT CONFLICT 214 214 L -> V (IN REF. 4).
CC FT CONFLICT 214 214 E -> K (IN REF. 2).
CC SQ SEQUENCE 240 AA; 26351 MW; 49DOB67E1390B39 CRC64;

Query Match 10.8%; Score 159.5; DB 1; Length 240;
Best Local Similarity 23.8%; Pred. No. 4.6e-06;
Matches 53; Conservative 41; Mismatches 66; Indels 63; Gaps 9;

QY 79 QVQWQLRQLVRKMLRTSBETISTVQEKQON-ISPLVRERGPRVAAHITGTRGNTLS 137
Db 60 QLHWRLGEMVTRLPDGPAGSWEQLIGERSHEVNP-----AAHLTGANSSLTGSG 109
QY 138 SPNSKNEKALGRKINSWSSRSRSHSPLSNHLRNGELVIHEKGFYIYSQTVRFQBEIK 197
Db 110 GP-----LLWE-TOLGLAFLRGLSYHDGALVVTAKAGYVYISK----- 146
QY 198 ENTENDKQMVQY-----LYKYT-SYDPDPIILLMKSAENSCWSKDAEYGLY 240
Db 147 -----VQLGGVCCPLGLASTITHGYKTPRYPEELELLVSSQSPCGRATSSSRV 197
QY 241 --SYQGGIFELKENDRIFVSVNTHLDM-DHEASFFGAFV 280
Db 198 WDSFLGGVYVHLEAGEVVVRLDERLRLRDTGTSYFGAFV 240

Search completed: March 23, 2004, 09:05:48
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:03 ; Search time 45 Seconds
(without alignments)
1970.236 Million cell updates/sec

Title: US-10-662-429-2
Perfect score: 1478
Sequence: 1 MAMMEVQGGPSLGTCVLIV.....NEHLIDMDEASFFGAFLVG 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeo:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	963	65.2	287	11	Q8K3G0
2	809.5	54.8	304	13	Q7TIF2
3	334.5	22.6	317	13	Q7ZVX9
4	307.5	20.8	287	13	Q90WT9
5	305.5	20.7	214	13	Q9DDZ5
6	184.5	12.5	279	11	Q7TIV9
7	180	12.2	252	11	Q8K3Y8
8	178.5	12.1	280	6	Q861W5
9	175.5	11.9	169	11	Q9WV90
10	175	11.8	252	11	Q80Y20
11	173	11.7	252	11	Q8K3Y7
12	166	11.2	251	4	Q8NFE9
13	157	10.6	154	6	Q8MJ19
14	153.5	10.4	227	13	Q7T2Q3
15	144.5	9.8	216	11	O70332
16	141	9.5	231	13	Q8AW02

17	137.5	9.3	232	11	Q80XA4
18	135	9.1	156	11	Q91ZL4
19	135	9.1	215	6	Q9BEE8
20	135	9.1	217	11	Q9ERG6
21	130.5	8.8	222	13	Q7T1U4
22	130.5	8.8	225	13	Q91B41
23	130.5	8.8	225	13	Q91B42
24	128	8.7	230	13	Q8JG37
25	127	8.6	253	13	Q7T194
26	126.5	8.6	215	11	Q99ND1
27	124	8.4	216	6	Q9BEC4
28	123.5	8.4	216	6	Q9BEC9
29	122	8.3	205	4	Q8M4C3
30	121.5	8.2	246	13	Q91976
31	121.5	8.2	246	13	Q91970
32	120	8.1	237	13	Q8AWC9
33	119	8.1	202	11	Q80WE7
34	116.5	7.9	217	6	Q9BEG0
35	116.5	7.9	217	6	Q9BEF4
36	115.5	7.8	149	6	Q97543
37	113.5	7.7	255	13	Q918I0
38	113.5	7.7	255	13	Q9DEP9
39	112.5	7.6	217	6	Q9BEG1
40	112.5	7.6	638	8	Q9Z2W6
41	110	7.4	93	6	Q9T1J2
42	109.5	7.4	149	6	Q97538
43	109.5	7.4	149	6	Q9T7G8
44	109	7.4	288	13	Q8JHJ4
45	109	7.4	652	11	Q60421

ALIGNMENTS

RESULT 1

Q8K3G0 PRELIMINARY; PRT; 287 AA.

AC Q8K3G0; DT 01-OCT-2002 (TREMREL. 22, Created)

DT 01-OCT-2002 (TREMREL. 22, Last sequence update)

DT 01-OCT-2003 (TREMREL. 25, Last annotation update)

DE TNF-related apoptosis inducing ligand.

OS Rattus norvegicus (Rat).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DA;

RA Mueller A.M., Giegerich G.;

RT "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY115578; AAM49797.1; -

DR GO; GO:0016020; C-membrane; IEA.

DR GO; GO:0005164; F-tumor necrosis factor receptor binding; IEA.

DR GO; GO:0006955; P-immune response; IEA.

DR InterPro; IPR006052; TNF family.

DR InterPro; IPR008983; TNF like.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD002012; TNF subf. 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF 1; 1.

DR PROSITE; PS0049; TNF 2; 1.

SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 65.2%; Score 963; DB 11; Length 287;

Best Local Similarity 67.7%; Pred. No. 2.7e-72;

Matches 189; Conservative 29; Mismatches 51; Indels 10; Gaps 3;

QY 9 GPSLQG---TCVLIVIFVTLLQSLCVAVTYVYFTNELKQMDKYSKSGIACFLKEDDSY 64

Db 9 GFSFSQHFMTVICIVLLQVLQAVTYVYFNNVAKLQDNYSKIGLACFSKEDGDF 68

```
QY 65 WDPNDESMNSPCQVQWQQLRQLVRKMLRTSSETISTVQEKQONTSPILVRERGQVAA 124
DB 69 WDSDEGILNRPCLQVKRQYQLIEEVLTKFTKISTVPEKQLSTPPLRGRRPQVAA 128
QY 125 HITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIT 184
DB 129 HITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIT 188
QY 185 YSQTYFRFQF--BIKENTKND-----KQVQYIYKYTSYPPILLMKSARNSCWSKDAEYX 238
DB 189 YSQTYFRFKEAKASKTVSKDGRKIKOMQVYIYKYTSYPPILLMKSARNSCWSREAYG 248
QY 239 LYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGA 277
DB 249 LYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGA 287

RESULT 2
Q7T1F2 PRELIMINARY; PRT; 304 AA.
AC Q7T1F2;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN TRAIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Sayed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;
RT "Identification and Characterization of Chicken TNF-superfamily
RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
RT Inducing Ligand TRAIL).";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB114678; BAC79267.1; -.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.8%; Score 809.5; DB 13; Length 304;
Best Local Similarity 55.4%; Pred. No. 1.9e-59;
Matches 160; Conservative 45; Mismatches 65; Indels 19; Gaps 6;

QY 8 GGSLSGQTCVLIIVITVLLQSLCAVAVTYVFTNELKQMDKYKSGIACFLKEDDSYWP 67
DB 5 GGSPPARTCGAVLVAALLQSVCAVAVTYVFTNELKQMDKYKSGIACFLKEDDSYWP 64
QY 68 N-----DESMNSPCQVQWQQLRQLVRKMLRTSSETISTVQ-EKQONTSPILVRERGQ- 120
DB 65 NLDVBSKDRVADPCQVQWHLGKLIKQMSRILQENMSAINDRGTQALS--RDEFPQ 122
QY 121 ---RVAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELVTH 177
DB 123 PTLRIAAHTGSKRSASA-SPHNYLSYRGIGIKIHSWESSRSGHSLYVNLWNGELVLP 181
QY 178 EKGFYIYQTYFRFQF-----IKENTKNDKQVQYIYKYTSYPPILLMKSARNSCW 231
DB 182 QTGFYIYQTYFRFQFRENEDSGLLERIKNPQVQYIYKLTNYPPILLMKSARTSCW 241
QY 232 SKDAEGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLV 280
DB 242 SKKAEGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAFMI 290

RESULT 3
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC Q7ZYX9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
```

```
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Similar to tumor necrosis factor (Ligand) superfamily, member 10.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044336; AAH44336.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 22.6%; Score 334.5; DB 13; Length 317;
Best Local Similarity 29.2%; Pred. No. 8.7e-20;
Matches 83; Conservative 55; Mismatches 113; Indels 33; Gaps 8;

QY 18 LVIIVTLLQSLCAVAVTYVFTNELKQMDKYKSGIACF-----LKEDDSYWDND-EE 71
DB 40 MVIVVVLQIASTTGLFVILNLSQVKSQVTELRCLGLNLVGLKQDI--PEDLAQ 97
QY 72 SMNSPCQVQWQQLRQLVRKMLRTSSETISTVQEKQONTSPILVRERGQ 120
DB 98 LRGEPCMKLAEGIKAVISKVTDLSIKQTLHAARTHTSYNTTSGKFTTV-----MQ 150
QY 121 RVAHITGTRGNT-----LSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGELV 175
DB 151 RPSAHLTLSSASDNRQSDMHQPQFDLHSCRFVHTW-ANKSFGAHLNNTLTNGRLR 209
QY 176 IHEKGFYIYQTYFRF-QEIKENTKNDKQVQYIYKYTSYPPILLMKSARNSCWSK 234
DB 210 VPQDERYLYSQVYFRYPSPSDQSSVSHQVLCVYIKKTSYLNFIQLLKGVTKWAPD 269
QY 235 AEYGLYSIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAF 278
DB 270 AEYALHSYVQGGIFELRAGDEVFVSVGPTVMYVGEDSSSYFGAF 313

RESULT 4
Q90WT9 PRELIMINARY; PRT; 287 AA.
AC Q90WT9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
RT ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AAL23702.1; -.
DR HSSP; O35235; 11QA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
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DR GO: GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PSS0049; TNF_2; 1.
DR SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match 20.8%; Score 307.5; DB 13; Length 287;
Best Local Similarity 32.3%; Pred. No. 1.4e-17;
Matches 93; Conservative 46; Mismatches 110; Indels 39; Gaps 11;

QY 18 LIVIFTVLQ--SLCVATVYVFT-----NELQM--QDKYSKSGIACPLEKDDSYWD 66
Db 8 LHAFFSLQLPLCTAPEAAGTWSQALQGNAPFLPKAQSQSSEELCLIQINQQEG 67

QY 67 PNDEESM-NSPFCMVQKQLQVKEKMLRTSEETI--STVQEKQ---NISP-LVRERGP 119
Db 68 SNLEELISQSC---LKLANTIKAYATVTENVISRVNEAKGSFVNISEGVQVATKL 123

QY 120 QRVAAHI-----TGTGRSNTLSSPNKNEKALGRKINSWESSRSCHSFISNHLR 170
Db 124 GKPSNHLIFRPQNPADQSGSRRFGNLS-----QSCRHAITRWEDS-TIHSHLQNTYR 175

QY 171 NGELVLTHEKGFYIYSOTYFRFOEIEIKENTKNDKQVQYIVKYTSPDPILLMKARNSC 230
Db 176 DGLRLVNQAGKYVYYSIYFRYSDGAGARVSPQLVQCINWKTYSQPIILLKGVTKC 235

QY 231 WSKDAEYGLYSIYQGGLFELKENDRIFVSVTNEHLIDMDHEAGFFGAF 278
Db 236 WAPAEYGLHLYQGGLFELKAGDELFVSYSLLAIDYSDAASVFGAF 283

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RESULT 5
Q9DDZ5      PRELIMINARY;      PRT;      214 AA.
AC Q9DDZ5;
DT 01-WAR-2001 (TReMBLrel. 16, Created)
DT 01-WAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE TRAIL-like protein.
GN TNFSF10L.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]_TaxID=7955;
SEQUENCE FROM N.A.
RA Boe J., Goetz F.W.;
RP "Molecular cloning and expression of a TNF receptor and two TNF
RT ligands in the fish ovary.";
RT Comp. Biochem. Physiol B, Comp. Biochem. 129:475-481(2001).
RL EMBL: AF250041; AAG47640.1; -.
DR HSSP; P50591; ID2Q.
DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_subf.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF; 1.
DR PROSITE; PS00049; TNF; 1.
SQ SEQUENCE      214 AA; 24093 MW;  98C002474F691AA  CRC64;
Query Match      20.7%; Score 305.5; DB 13; Length 214;

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[illegible]

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Db 202 NQFLNKKVNRNKKYPEDLVMEKRLNYCTT--GQIWAHSHLGAFFNLTSAHLYVNI 259
QY 261 TNEHLIDMDHEASFFGAF 278
Db 260 SLSLINFESKTFFGLY 277

RESULT 7
Q8K3Y8 ID Q8K3Y8 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y8
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TLIA.
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=21909416; PubMed=11911831;
RA Magone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakara P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Fukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TLIA is a TNF-like ligand for DR3 and TR6/DCR3 and functions as a T
RT cell costimulator.";
RL Immunity 16:479-492(2002).
DR ENBL; AF520786; AA07367.1; -.
DR MGD; MGI:2180140; Tnfslf15.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;

Query Match 12.2%; Score 180; DB 11; Length 252;
Best Local Similarity 32.4%; Pred. No. 5.1e-07;
Matches 69; Conservative 26; Mismatches 80; Indels 38; Gaps 12;

QY 83 QLRVQRKMLRTSEETISTVQEKQKQINSLPLVRERGQPVAAHITGTRGNTLSSPSNK 142
Db 63 QLRVPGKCDMLRAITTEERSE--PSPQVYSP---PRGKPR--AHLT-----IKKQTPAHLK 112
QY 143 NE-KALGRKINSWESSRSGHSLN-LHLRNGELVHEKGFYIYSQTYRFQEEI---- 196
Db 113 NQLSAL-----HWEDH-LGWAFTNGMKYINKSLVIFESGDYFIYSQITRGTTSCVDI 166
QY 197 ---KENTKNDKQMVQIYKYTSYDPDILLMKASRNSC-----WSKDAEYGLYSIQGIF 248
Db 167 SGRGRPNKPSITVITKADSYEPARLLTGSVCEISNNW-----FQSIYLGAMP 219
QY 249 ELKENDRIFVSTNEHLIDMDHE--ASFGAPLV 280
Db 220 SLEEGRLMNVSDISLVDTYKEDTKTFGAPLL 252

RESULT 8
Q861W5 ID Q861W5 PRELIMINARY; PRT; 280 AA.
AC Q861W5;
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DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fas ligand.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99053606; PubMed=9839871;
RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Tsubota K.,
RA Mikami T., Ohno K., Watari T., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs.";
RL Vet. Immunol. Immunopathol. 65:161-172(1998).
DR ENBL; AB009280; BAC76426.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SEQUENCE 280 AA; 31361 MW; 6AA7E2DE1F1A6B5C CRC64;

Query Match 12.1%; Score 178.5; DB 6; Length 280;
Best Local Similarity 21.2%; Pred. No. 7.7e-07;
Matches 58; Conservative 53; Mismatches 77; Indels 85; Gaps 11;

QY 16 CVLIVFTVLLQSLCVAV---TVVYPTNELKQMDKYSKSGIACFLKEDSDYDPNDES 72
Db 81 CLLVMEFFVLVALVGLGFMFLHQLKELARESTSQHVASSLEKQIGQLNPSEK- 139
QY 73 MNSPCQVQKQLRQLVRKMLRTSEETISTVQEKQKQINSLPLVRERGQPVAAHITGTR 132
Db 140 -----REL-----RKLVAHLTG----- 150
QY 133 SNTLSSPSNKKALGRKINSWESSRSGHSLNHLRNGELVHEKGFYIYSQTYRPF 192
Db 151 -----KPNRSIPL-----EWEDT-YGIALVSGVKYKGGVLINDTGMVYFYSKVNFRG 198
QY 193 QBEIKENTKNDKQMVQIY-KYTSYDPDILLMK-SARNSC-----WSKDAEYGLYSIQG 245
Db 199 Q-----SCNNQPLNHKVYRNRSKYPDVLVMEGKMNCTTGQMMAR-----SSYL 245
QY 246 GFELKENDRIFVSTNEHLIDMDHEASFGAF 278
Db 246 AVFNLTSAHLYVNVNSELVSVFESKTFFGLY 278

RESULT 9
Q9WF90 ID Q9WF90 PRELIMINARY; PRT; 169 AA.
AC Q9WF90
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fas ligand (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scluridae; Sciurinae;
OC Marmota.
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OX NCBI_TaxID=9995;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20010026; PubMed=10540161;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RL chronic woodchuck viral hepatitis."
RL Clin. Exp. Immunol. 118:63-70(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR HSSP; P50591; 1D4V.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON TER 1
FT NON TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 11.9%; Score 175.5; DB 11; Length 169;
Best Local Similarity 27.8%; Pred. No. 7.2e-07;
Matches 54; Conservative 39; Mismatches 58; Indels 43; Gaps 10;

QY 83 QLRQVVKMLRTSEETISTVQEKQNIPLVREGRQORVAAHITGTRGSNTLSSPNSK 142
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 10 ELRESINQ---RNTPELS---EQIGHPSPSDKALRAAHIT---GKPNSSSP--- 56
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 143 NEKALGRKINSWESSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRQEEIKENTKN 202
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 57 -----LEWEDT-YGISLSGVKYQKGLVINDTGLYFVSKYIFRGQ-----SCN 100
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 203 DKQMVQIY-KYTSYPPDILMK-SARNSC-----WSKDAEYGLYSYQGGIFELKENDR 255
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 101 NQPLSHKVVYKNSKYQDQLVMEKGKNNYCTTGQWAR-----SSYLGAVFNF--SNDH 153
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 256 IFVSVTNEHLIDMD 269
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 154 LYVNVSELSLNEF 167
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 10
Q80YZ0
ID Q80YZ0 PRELIMINARY; PRT; 252 AA.
AC Q80YZ0
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BN20K13.3 (tumor necrosis factor (ligand) superfamily, member 15).
DE TNFSF15.
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA Sycamore N.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL691468; CAD83021.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_subf.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789E6556D46F293 CRC64;

Query Match 11.7%; Score 173; DB 11; Length 252;

DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_subf.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27725 MW; A63ABDDCC9E969E0F CRC64;

Query Match 11.8%; Score 175; DB 11; Length 252;
Best Local Similarity 31.9%; Pred. No. 1.3e-06;
Matches 68; Conservative 26; Mismatches 81; Indels 38; Gaps 12;

QY 83 QLRQVVKMLRTSEETISTVQEKQNIPLVREGRQORVAAHITGTRGSNTLSSPNSK 142
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 63 QLRVPGKDCMLRAITEERSE-PSPOQVYSP---PRGKPR-AHLT-----IKKQTPAPHLK 112
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 143 NE-KALGRKINSWESSRSGHSLN-LHLRNGELVTHEKGFYIYSQTYFRQEEI----- 196
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 113 NQLSAL-----HNEHD-LGWAFTKNGKYLKSLVPESGDIYISQITFRGTSVCGDI 166
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 197 ---KENTKNDKQMVQIYKYTSYPPDILMK-SARNSC-----WSKDAEYGLYSYQGGIF 248
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 167 SRGRPNKPSITWITTKVADSYPEPARLLTGTSGKSVCEISNNW-----FQSLYLGA 219
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 249 ELKENDRIFVSVTNEHLIDMDHE-ASFFGAPLV 280
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:
QY 220 SLEEDRLMVNVSDISLVDYTKEDTKTFGFAFL 252
Db :||: : : : : ||| :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 11
Q8K3Y7
ID Q8K3Y7 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TL1A.
DE TNFSF15.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21909416; PubMed=11911831;
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TL1A is a TNF-like ligand for DR3 and TR6/DCR3 and functions as a T
cell costimulator."
RL Immunity 16:479-492(2002).
DR EMBL; AF520787; AA077368.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_subf.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789E6556D46F293 CRC64;

Query Match 11.7%; Score 173; DB 11; Length 252;
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Best Local Similarity 32.7%; Pred. No. 1.9e-06;
Matches 56; Conservative 23; Mismatches 62; Indels 30; Gaps 8;

QY 124 AHLTGTGRGNTLSSPNKNEKALGRKINSWSSRSGHSFLSN-LHLRNGELVHEKGFY 182
Db 98 AHLTGTGRGNTLSSPNKNEKALGRKINSWSSRSGHSFLSN-LHLRNGELVHEKGFY 182
QY 183 YIYSQTVFRFQ-----EIKENTKNDKQVQYIYKYTSYPPILLMKSARNSC----- 230
Db 149 FIYSQITFRGTTSECGDISRVRPKPDSITVITKVDSPPEPAHLLTGTKSVCEISSN 208
QY 231 WSKDAEGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHE-ASFQGAFLV 280
Db 209 W-----FOPIYLGAMFSLSEGRMLMVNSDISLVDTYTKEDKTFFGAFLI 252

RESULT 12
Q8NF99 PRELIMINARY; PRT; 251 AA.
AC Q8NF99;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
GN TNF superfamily ligand TLIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21909416; PubMed=11911831;
RA Mgione T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakara J.P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Fukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RA "TLIA is a TNF-like ligand for DR3 and TR6/DCR3 and functions as a T
RT cell costimulator.";
RL Immunity 16:479-492(2002).
DR EMBL; AF520785; AAM7366.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_abc;
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 251 AA; 28087 MW; 65ED70E367E3446D CRC64;

Query Match 11.2%; Score 166; DB 4; Length 251;
Best Local Similarity 33.2%; Pred. No. 7.4e-06;
Matches 62; Conservative 30; Mismatches 55; Indels 30; Gaps 12;

QY 107 QONISPLVRGPGORVAAHITGTRGNTLSSPNKNE-KALGRKINSWSSRSGHSFLS 165
Db 82 QQVYAPLRADGDKPR--AHLTVR-----QTPTQHFKNQFPAL-----HWE-HELGLAFTK 129
QY 166 N-LHLRNGELVHEKGFYIYQYVFRFQ-----EIKENTKNDK--QMVGYYIKYT-SYP 217
Db 130 NRMVYTKFLIPESGDYFIYSQVTFRGMTSECEIQAGRPKNPKDSITVITKVDTSYP 189
QY 218 DPILLMKSARNCSWSDAEYXG---LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE-AS 273
Db 190 EPTQLMGTKSVG-----EVGSNWFQPIYLGAMFSLQEGKLMVNSDISLVDTYTKEDKT 244
QY 274 FFGAFLV 280
Db 245 FFGAFLI 251
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RESULT 13
Q8MJ19 PRELIMINARY; PRT; 154 AA.
AC Q8MJ19;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fas ligand CD178 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530076; AAM95636.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008084; Fas_ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779B029449 CRC64;

Query Match 10.6%; Score 157; DB 6; Length 154;
Best Local Similarity 27.4%; Pred. No. 2.2e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;

QY 95 TSEETISTVQEKQONISPLVRGPGORVAAHITGTRGNTLSSPNKNEKALGRKINSW 154
Db 8 TSQKHTASLSEKQIGHPSPPPEKQKQKVAHLTG-----KPNRSRSMPL-----EW 52
QY 155 ESSRSRSGHSFLSNLHLRNGELVHEKGFYIYQYVFRFQEEIKENTKNDKQVQYIY-KY 213
Db 53 EOT-YGIVLLSGVKYKGGVLINETGLYFYYSKVFRGQ-----SCTNLPISHKVMRN 105
QY 214 TSYPDPIILLMKSARNCSWSDAEYGLYIYQGGIFELKENDRIFSVT 261
Db 106 SKYPQDLVNMVEGKQWS-YCTTGQMWASHSYLGAVENTLTSADHLVNVVS 152

RESULT 14
Q7T2Q3 PRELIMINARY; PRT; 227 AA.
AC Q7T2Q3;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor-3 alpha.
GN TNF-3ALPHA.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```

RESULT 15
ID 070332 PRELIMINARY; PRT; 216 AA.
ID 070332;
AC 070332;
DT 01-AUG-1998 (trEMBLrel. 07, Created)
DT 01-AUG-1998 (trEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (trEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
[1]_TaxID=10036;
SEQUENCE FROM N.A.
RP RP
RX TISSUE=Spleen;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tyvon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998) .
DR EMBL; AF046215; RAC40100.1; -.
DR HSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR Prodom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 09:04:02 ; Search time 60 Seconds
(without alignments)
1323.264 Million cell updates/sec

Title: US-10-662-429-2

Perfect score: 1478

Sequence: 1 MAMMEVGGPSLGTCTVLIV.....NEHLIDMDHEASFGAFLVG 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1478	100.0	281	2 AAW19777	Novel cyt
2	1478	100.0	281	2 AAW27134	Human apo
3	1478	100.0	281	2 AAW19787	Human apo
4	1478	100.0	281	2 AAW76829	Human TL2
5	1478	100.0	281	2 AAW56760	Human TRA
6	1478	100.0	281	2 AAW44354	Human AGP
7	1478	100.0	281	2 AAY01517	Protein a
8	1478	100.0	281	2 AAY27012	Human Apo
9	1478	100.0	281	3 AAY81956	Human Apo
10	1478	100.0	281	3 AAB24038	Human PRO
11	1478	100.0	281	3 AAB08545	Amino aci
12	1478	100.0	281	3 AAB28691	Human AGP
13	1478	100.0	281	4 AAB50977	Human PRO
14	1478	100.0	281	4 AAB67243	Human Apo
15	1478	100.0	281	4 AAE11031	Human TNF
16	1478	100.0	281	4 AAB48350	Human TL2
17	1478	100.0	281	5 ABB08133	Human TRA
18	1478	100.0	281	5 ABG31630	Human TRA
19	1478	100.0	281	5 AAU75062	Human TNF
20	1478	100.0	281	5 AAMS1077	Human Apo
21	1478	100.0	281	5 ABP51954	Human Apo
22	1478	100.0	281	5 AAO19095	C neoform
23	1478	100.0	281	5 AAU79593	Human TNF
24	1478	100.0	281	6 ABG73861	Human Apo
25	1478	100.0	281	6 ABU10205	Human Apo

26	1478	100.0	281	6 ABU71443	Human neo
27	1478	100.0	281	6 ABG72738	Human TNF
28	1478	100.0	281	6 AAO29543	Human TRA
29	1478	100.0	281	6 ABU08558	Human TNF
30	1478	100.0	281	6 ABR42313	Human TRA
31	1478	100.0	281	6 ABG71905	Human TRA
32	1478	100.0	281	6 ABP60546	Human tum
33	1478	100.0	281	6 AAE36258	Human TRA
34	1478	100.0	281	6 AAO31151	Human TNF
35	1478	100.0	281	6 ABO25125	Human TNF
36	1478	100.0	281	7 ADB61471	Native hu
37	1478	100.0	281	7 ADC35202	Human TNF
38	1478	100.0	281	7 ADD14080	Human src
39	1478	100.0	281	7 ADD19010	Human dis
40	1478	100.0	281	8 ADE76953	Human pro
41	1475	99.8	281	7 ADB61488	Human Apo
42	1473	99.7	281	5 ABG72257	Human tum
43	1473	99.7	281	7 ADB61478	Human Apo
44	1473	99.7	281	7 ADB61477	Human Apo
45	1473	99.7	281	7 ADB61479	Human Apo

ALIGNMENTS

RESULT 1

AAW19777
ID AAW19777 standard; protein; 281 AA.

XX AAW19777;

DT 22-SEP-1997 (first entry)

XX Novel cytokine Apo-2 ligand.

DE Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..281
FT /note= "Claim 4"
FT Region 1..14
FT /label= Cytoplasmic_region
FT Protein 15..281
FT /note= "Claim 3"
FT Region 15..40
FT /label= Transmembrane_region
FT Protein 41..281
FT /note= "Claim 2"
FT Region 41..281
FT /label= Extracellular_region
FT Modified-site 109
FT /label= Glycosylation
FT Protein 114..281
FT /note= "putative N-linked glycosylation site"
FT /note= "Claim 1"

WO9725428-A1.

17-JUL-1997.

08-JAN-1997; 97WO-US000272.

09-JAN-1996; 96US-00584031.

(GETH) GENENTECH INC.

Ashkenazi AJ, Chuntharapai A, Kim KJ;

WPI; 1997-372867/34.

N-PSDB; AAW72796.

PT Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
PT apoptosis for the treatment of breast and colon cancer.
XX Claim 4; Fig 1a; 72pp; English.
XX
CC A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian
CC cell apoptosis. It is believed to be a member of the tumour necrosis
CC factor cytokine family. Its amino acid sequence was deduced from a cDNA
CC clone (AAW72796) isolated from a human placental cDNA library. Apo-2
CC ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
CC 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
CC transformed or transfected with a vector contg. Apo-2 ligand nucleic
CC acid. They can be used to induce apoptosis in mammals and to treat
CC pathological conditions such as cancer (esp. breast or colon cancer) or
CC to raise antibodies useful in diagnostic assays
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180

QY 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 2
AAW27134
ID AAW27134 standard; protein; 281 AA.
XX
AC AAW27134;
XX
DT 02-APR-1998 (first entry)
XX
DE Human Apoptosis inducing molecule-I (AIM-I).
XX
KW Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
KW tumour necrosis factor ligand superfamily; AIM-I altered expression;
KW neoplasia inhibition; anti-inflammatory agent.
XX
OS Homo sapiens.
XX
FN WO9733899-A1.
XX
PD 18-SEP-1997.
XX
PF 14-MAR-1996; 96WO-US003773.
XX
PR 14-MAR-1996; 96WO-US003773.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM;
XX
DR WPI; 1997-470807/43.
DR N-PSDB; AAT85210.

XX New isolated apoptosis inducing molecule-I - used to develop products for
PT the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
PT versus host disease or inflammation.
XX
XX Claim 2; Fig 1; 82pp; English.
XX
CC The present sequence represents a human Apoptosis inducing molecule-I
CC (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand
CC superfamily. The products can be used in the diagnosis and treatment of
CC disorders related to under-expression, over-expression or altered
CC expression of AIM-I. AIM-I or agonists can be used for treating
CC autoimmune disorders including systemic lupus erythematosus,
CC immunoproliferative disease lymphadenopathy (IPL),
CC angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
CC diabetes, and multiple sclerosis, graft versus host disease, to inhibit
CC neoplasia such as tumour cell growth, to treat restenosis, to regulate
CC haematopoiesis in endothelial cell development, to stimulate peripheral
CC tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
CC used for treating cachexia, cerebral malaria, rheumatoid arthritis or
CC osteoporosis, for preventing graft-host rejection, and as anti-
CC inflammatory agents, for treating endotoxic shock or to prevent
CC activation of HIV
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60
DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCVAVTVYVFTNELKQMDKYSKSGIACFLKE 60

QY 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120
DB 61 DDSYWDNDDESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQONISPLVRERGPO 120

QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180
DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIEHGK 180

QY 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
DB 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 3
AAW19787
ID AAW19787 standard; protein; 281 AA.
XX
AC AAW19787;
XX
DT 24-SEP-1997 (first entry)
XX
DE Human apoptosis inducer cytokine TRAIL.
XX
KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
KW cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangioplasty; therapy.
XX
OS Homo sapiens.
XX
FN 1. .18
PI /label= Cytoplasmic_domain
FT Domain 19. .38
FT /label= Transmembrane_domain
FT Domain 39. .281

	/label= Extracellular_domain
	/note= "contains a receptor-binding region"
Cleavage-site	89..190
Modified-site	/note= "potential KEX2 protease processing site"
Cleavage-site	109..111
	/note= "potential N-glycosylation site"
Cleavage-site	149..150
	/note= "potential KEX2 protease processing site"
WO9701633-A1.	
16-JAN-1997.	
XX XX	
XX XX	25-JUN-1996; 96WO-US010895.
XX XX	29-JUN-1995; 95US-00496632.
XX XX	01-NOV-1995; 95US-00548368.
XX XX	(IMMV) IMMUNE CORP.
XX XX	Wiley SR, Goodwin RG;
XX XX	WPI; 1997-118715/11.
XX XX	N-PADB; AAT72847.
XX XX	TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral infection and for use in assays.
XX XX	Claim 10; Page 43-44; 62pp; English.
XX XX	Human tumour necrosis factor related apoptosis inducing ligand (TRAIL) (AAW19787) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AAW72848), deposited in vector pDC409 as ATCC 63849. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or to raise antibodies that may be useful for treating thrombotic microangiopathies
XX XX	Sequence 281 AA;
Query Match	100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity	100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 1	MAMMEVQGSPSLGQCCLIVIFVTLLQLSCVAVTVVFTNKLKOMODKYSGGIACFLKE 60
DB 1	MAMMEVQGSPSLGQCCLIVIFVTLLQLSCVAVTVVFTNKLKOMODKYSGGIACFLKE 60
QY 61	DSYNDPDNEESNMSPFCWKWLRLKVLRTSEETISTVQEKQNISPLVRERGPQ 120
DB 61	DSYNDPDNEESNMSPFCWKWLRLKVLRTSEETISTVQEKQNISPLVRERGPQ 120
QY 121	RVAAHITGRGSNTLSSPNKNKALGRKINSWESSRSHSFNLHRLNGELVIEHGK 180
DB 121	RVAAHITGRGSNTLSSPNKNKALGRKINSWESSRSHSFNLHRLNGELVIEHGK 180
QY 181	FYYIYSQTFRFQEIKENTKDKQMVOYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
DB 181	FYYIYSQTFRFQEIKENTKDKQMVOYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
QY 241	SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFLVG 281
DB 241	SIYQGGIFELKENDRIFFSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 4	
AAW76829	
ID AAW76829	standard; protein; 281 AA.
XX AC	AAW76829;

```

RESULT 5
AAW56760
ID AAW56760 standard; protein; 281 AA.
XX
AC AAW56760;
XX
DT 05-AUG-1998 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
KW cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..18
FT /note= "N-terminal cytoplasmic domain"
FT Region 19..38
FT /note= "transmembrane region"
FT Domain 39..281
FT /note= "extracellular domain"
XX
FN US5763223-A.
XX
PD 09-JUN-1998.
XX
PF 25-JUN-1996; 96US-00670354.
XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548369.
XX
FA (IMMV) IMMUNEX CORP.
XX
PI Goodwin RG, Wiley SR;
XX
WPI; 1998-347322/30.
XX
N-PSDB; AAV29518.
XX
DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
PT for producing recombinant polypeptides for research and therapy of
PT leukaemia, lymphoma, melanoma and viral infections.
XX
PS Claim 1; Col 33-36; 28pp; English.
XX
CC This represents a human tumour necrosis factor related apoptosis ligand
CC (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce
CC apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful
CC for producing the recombinant TRAIL polypeptides, which may be useful in
CC studies of apoptosis to purify leukaemia, lymphoma or melanoma cells
CC (e.g. to isolate antigens for vaccine development). The polypeptides can
CC be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal
CC treatment of blood or bone-marrow), or to treat viral infections
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVTVYVFTNLKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVTVYVFTNLKQMDKYKSGIACFLKE 60
QY 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQKQNIISPLVREGPQ 120
Db 61 DDSYWDPNDEESMNSPCQVQKQLRQLVRKMLRTSEETISTVQKQNIISPLVREGPQ 120
QY 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFTLNHLRNGELVITHEKG 180
Db 121 RVAAHITGRGNTLSSPNSKNEKALGRKINSWESSRSGHSFTLNHLRNGELVITHEKG 180

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QY 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRQBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 240
QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
RESULT 6
AAW44354
ID AAW44354 standard; protein; 281 AA.
XX
AC AAW44354;
XX
DT 28-MAY-1998 (first entry)
XX
DE Human AGP-1.
XX
KW Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation;
KW bone resorption; haematopoietic disease.
XX
OS Homo sapiens.
XX
FN WO9746686-A2.
XX
PD 11-DEC-1997.
XX
PF 06-JUN-1997; 97WO-US009895.
XX
PR 07-JUN-1996; 96US-00660562.
XX
FA (AMGE-) AMGEN INC.
XX
PI Johnson MJ, Simonet WS, Danilenko DM;
XX
WPI; 1998-042194/04.
XX
N-PSDB; AAV15295.
XX
Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein -
PT useful for treating inflammation, bone resorption and haematopoietic
PT diseases.
XX
PS Claim 7; Page 36-37; 54pp; English.
XX
CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis
CC factor (TNF)-related protein, involved in inflammation, myelopoiesis and
CC bone resorption. It has the same nucleic acid and amino acid (aa)
CC sequences as the TNF-related apoptosis-induced ligand (TRAIL) described
CC in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay
CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVTVYVFTNLKQMDKYKSGIACFLKE 60
Db 1 MAMMEVQGGPSLQGTCLVLIIVFTLLQSLCAVTVYVFTNLKQMDKYKSGIACFLKE 60

```

QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 7

AA01517
 ID AAY01517 standard; peptide; 281 AA.

AC AAY01517;

DT 27-MAY-1999 (first entry)

DE Protein associated with neurodegenerative and autoimmune diseases.

DE Neurodegenerative disease; autoimmune disease; inflammatory disease;
 KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
 KW surface receptor; TRAIL protein.

OS Homo sapiens.

XX FR2766713-A1.

XX 05-FEB-1999.

XX 04-AUG-1997; 97FR-00010176.

XX 04-AUG-1997; 97FR-00010176.

XX (INMR) BIO MERIEUX.

XX Rieger F, Belliveau JF, Perron H;

XX WPI; 1999-156177/14.

XX Use of polypeptide derived from TRAIL protein for diagnosis of
 PT degenerative disease - autoimmunity and inflammation, also useful in
 PT prevention or treatment, and similar use of corresponding ligand and
 PT nucleic acid.

XX Claim 2; Page 13; 21pp; French.

XX The specification describes the use a polypeptide corresponding to at
 CC least the primary sequence of part of the present sequence to produce a
 CC diagnostic, prophylactic or therapeutic composition useful in cases of
 CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
 CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
 CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
 CC nervous system cells, antigenic and specifically recognise the surface
 CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
 CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
 CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
 CC receptors, inhibiting formation of natural complex

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVQGGPSLQGTCLIVIFTVLLQSLCAVAVYVYFTNELKQMDQKYSKGIACFLKE 60

DB 1 MAMMEVQGGPSLQGTCLIVIFTVLLQSLCAVAVYVYFTNELKQMDQKYSKGIACFLKE 60
 QY 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 DB 61 DSYWDPNDEESMNSPCWQVKQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSOTYFRFOBEIKENTKNDKQVQYIYKYTSYDPDILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 8

AA027012

ID AAY27012 standard; protein; 281 AA.

AC AAY27012;

XX 24-SEP-1999 (first entry)

DE Human Apo-2 ligand (Apo-2L) polypeptide.

DE Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
 KW lupus; immune-mediated glomerular nephritis; human.

OS Homo sapiens.

XX WO9936535-A1.

XX 22-JUL-1999.

XX 15-JAN-1999; 99WO-US001039.

XX 15-JAN-1998; 98US-00007886.

XX 15-APR-1998; 98US-00060533.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Kelley RF, O'Connell MT, Pitti RM, Schwall RH;

XX WPI; 1999-444397/37.

XX N-PSDB; AAX86987.

XX A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.

XX Claim 1; Fig 1A; 86pp; English.

XX This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMMEVGGPSLGQTCVLIVIFVTLQSLCAVAVYVFTNELKQMDQKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVIFVTLQSLCAVAVYVFTNELKQMDQKYSKSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 DB 61 DDSYWDNDDESNMSPCWQVKQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 9
 AAY81956
 ID AAY81956 standard; protein; 281 AA.
 XX AC AAY81956;
 XX DT 10-JUL-2000 (first entry)
 XX DE Human Apo-2 ligand protein sequence.
 XX KW Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
 KW therapy; apoptosis; cancer.
 XX OS Homo sapiens.
 XX PN US6046048-A.
 XX PD 04-APR-2000.
 XX PF 08-JAN-1997; 97US-00780496.
 XX PR 09-JAN-1996; 96US-0009755P.
 XX PA (GETH) GENENTECH INC.
 XX PI Kim KJ, Ashkenazi AJ, Chuntharapai A;
 XX WPI; 2000-282690/24.
 XX N-PSDB; AAA07425.
 XX PT New isolated monoclonal antibodies having antigen specificity for Apo-2
 PT ligand, e.g. 2G6, 2E11 or 5C2, useful for detecting the expression of Apo
 PT -2 ligand serum, and for treating diseases associated with increased
 PT apoptosis.
 XX PS Claim 9; Fig 1a; 46pp; English.
 XX CC This sequence is the human Apo-2 ligand protein, which is recognised by
 CC monoclonal antibodies produced by the hybridoma cell lines of the
 CC invention. The hybridoma cell lines are deposited under the American Type
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
 CC tissues, or serum. The antibodies may also be employed as therapeutics.
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
 CC pathological conditions or diseases associated with increased apoptosis.
 CC They are also useful for the affinity purification of Apo-2 ligand from
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells.
 XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGQTCVLIVIFVTLQSLCAVAVYVFTNELKQMDQKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGQTCVLIVIFVTLQSLCAVAVYVFTNELKQMDQKYSKSGIACFLKE 60
 QY 61 DDSYWDNDDESNMSPCWQVKQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 DB 61 DDSYWDNDDESNMSPCWQVKQLRQVLRKMLRTSEETISTVQEKQONISPLVRERGPQ 120
 QY 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSCWSDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 RESULT 10
 AAB24038
 ID AAB24038 standard; protein; 281 AA.
 XX AC AAB24038;
 XX DT 25-JAN-2001 (first entry)
 XX DE Human PRO1096 protein sequence SEQ ID NO:51.
 XX KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumorigenesis; anticancer; detection.
 XX OS Homo sapiens.
 XX PN WO2000053750-A1.
 XX PD 14-SEP-2000.
 XX PF 02-DEC-1999; 99WO-US028551.
 XX PR 08-MAR-1999; 99WO-US005028.
 XX PR 01-SEP-1999; 99WO-US020111.
 XX PR 29-OCT-1999; 99US-0162506P.
 XX PR 30-NOV-1999; 99WO-US028313.
 XX PR 01-DEC-1999; 99WO-US028634.
 XX PA (GETH) GENENTECH INC.
 XX PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
 XX WPI; 2000-594320/56.
 XX N-PSDB; AAC58120.
 XX PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
 PT the growth of tumors in mammals, and to identify inhibitors of PRO
 PT polypeptide activity or expression.
 XX PS Claim 61; Fig 36; 226pp; English.
 XX CC The present invention describes an antibody that binds to a human protein
 CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
 CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
 CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
 CC activity and can be used to diagnose tumours in mammals, by detecting
 CC complex formation when the antibody is contacted with test cells.
 CC Increased expression of genes encoding (I) can also be detected to

CC diagnose tumours. Agents which inhibit the activity of (I), especially
 CC the antibodies, or an antisense oligonucleotide which hybridises to genes
 CC encoding (I), can be used to inhibit tumour growth, preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (I). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAC24021 to AAC24040 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 DB 61 DDSYWDPNDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 11
 AAB08545
 ID AAB08545 standard; protein; 281 AA.
 AC AAB08545;
 XX
 DT 20-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a human TRAIL polypeptide.
 XX
 KW Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
 KW TNF related apoptosis-inducing ligand; tumour cell;
 KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
 KW non-small cell lung carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN W0200048619-A1.
 XX
 PD 24-AUG-2000.
 XX
 PF 15-FEB-2000; 2000WO-US003891.
 XX
 PR 16-FEB-1999; 99US-0120313P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Rosen GD;
 XX
 DR WPI; 2000-558253/51.
 DR N-PSDB; AAA64325.
 XX
 PT Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
 PT administration of synergistic combination of diterpenoid diepoxide and
 PT tumor necrosis factor related apoptosis-inducing ligand.
 XX

PS Disclosure; Page 23-24; 29pp; English.
 XX
 CC The present sequence represents a human TRAIL (tumour necrosis factor
 CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
 CC describes a method for enhanced killing of tumour cells. The method
 CC comprises contacting a susceptible tumour cell with a synergistic mixture
 CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
 CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
 CC and so is active at lower doses and against otherwise resistant cell
 CC lines. The method is used for killing tumour cells, especially solid
 CC tumours or carcinomas (especially mammary carcinoma or non-small cell
 CC lung carcinoma)
 XX
 SQ Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 DB 1 MAMMEVGGPSLGGTCLVLIIVFTVLLQSLCAVAVTVVFTNELKQMDKYSKSGIACFLKE 60
 QY 61 DDSYWDPNDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 DB 61 DDSYWDPNDESNMSPCWQVKWQLRQLVRKMLRTSEETISTVQEKQONISPLVREGPQ 120
 QY 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 DB 121 RVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHEKG 180
 QY 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 DB 181 FYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 DB 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 12
 AAB28691
 ID AAB28691 standard; protein; 281 AA.
 AC AAB28691;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Human AGP-1.
 XX
 KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
 KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 KW transplant rejection; cardiovascular disease; arteriosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN W0200063253-A1.
 XX
 PD 26-OCT-2000.
 XX
 PR 24-MAR-2000; 2000WO-US008004.
 XX
 PF 16-APR-1999; 99US-00293245.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Hsu H, Meng S;
 XX
 DR WPI; 2000-665240/64.
 DR N-PSDB; AAC67831.
 XX

PT Fusion protein of AGP-1 protein and an Fc region, used to treat
 PT proliferative disorders, immune disorders, and virally-induced disorders.

XX Claim 3; Fig 2; 93pp; English.

XX The present sequence is human AGP-1, a type II transmembrane protein.
 CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
 CC terminal portion of the AGP-1 protein have been produced. The fusion
 CC proteins can be used to induce apoptosis in a tissue, and to treat
 CC proliferative disorders, immune disorders, or virally-induced disorders.
 CC The proliferative disorders include cancers, such as breast, prostate,
 CC lung or colon cancer. The viral infections include hepatitis, and
 CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
 CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
 CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
 CC proteins have increased biological activity compared to the soluble AGP-1
 CC proteins used in prior art therapies

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-137;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Db 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60
 Qy 61 DDSYWDPNDESMNSPCQVQKWLRLVRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 Db 61 DDSYWDPNDESMNSPCQVQKWLRLVRKMLRTSEETISTVQEKQNIPLVREGPQ 120
 Qy 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180
 Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSDAEYGLY 240
 Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSDAEYGLY 240
 Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
 Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 13
 AAB50977
 ID AAB50977 standard; protein; 281 AA.

XX AAB50977;

DT 21-MAR-2001 (first entry)

XX Human PRO1096 protein.

XX Human; PRO; cytostatic; neutropic; neuroprotective; respiratory general;
 KW antinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

XX Homo sapiens.

XX WO200073348-A2.

XX 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-1999; 99WO-US012252.

XX 22-JUN-1999; 99US-014650P.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 03-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.

(GETH) GENENTECH INC.

Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 Shelton DL, Smith V, Watanabe CK, Wood WI;

WPI: 2001-016509/02.

N-PSDB; AAC91579.

XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for
 PT treating various tumors, e.g. breast cancer, and other inflammatory,
 PT angiogenic and immunological disorders.

XX Claim 31; Fig 54; 188pp; English.

XX The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumors, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoealic disorders, and inflammatory, angiogenic and immunological
 CC disorders

XX Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.6e-137;

Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60

Db 1 MAMMEVQGGPSLGTQCVLIIVFTVLLQSLCAVAVTVYFTNELKQMDKYKSGIACFLKE 60

Qy 61 DDSYWDPNDESMNSPCQVQKWLRLVRKMLRTSEETISTVQEKQNIPLVREGPQ 120

Db 61 DDSYWDPNDESMNSPCQVQKWLRLVRKMLRTSEETISTVQEKQNIPLVREGPQ 120

Qy 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Db 121 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHGK 180

Qy 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSDAEYGLY 240

Db 181 FYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYPPDILLMKSARNSCWSDAEYGLY 240

Qy 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

RESULT 14

AAB67243

ID AAB67243 standard; protein; 281 AA.

```

XX AC AAB67243;
XX DT 18-APR-2001 (first entry)
XX DE Human Apo2 ligand.
XX KW Human; Apo2 ligand; divalent metal ions; viral infection; cancer.
XX OS Homo sapiens.
XX PN WO200100832-A1.
XX PD 04-JAN-2001.
XX PF 26-JUN-2000; 2000WO-US017579.
XX PR 28-JUN-1999; 99US-0141342P.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
XX PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX DR WPI; 2001-123012/13.
XX DT Use of divalent metal ions for making Apo-2 ligand and in formulations
XX PT containing Apo-2 ligand for increasing yield and stability of ligand
XX PT trimers, useful for therapeutic applications.
XX PS Claim 6; Fig 1; 60pp; English.
XX CC The present invention relates to a formulation comprising Apo-2 ligand
XX CC and divalent metal ions. Apo-2 ligand and the formulation are useful for
XX CC treating cancers and viral infections. Addition of divalent metal ions
XX CC for making Apo-2 ligand and formulations containing Apo-2 ligand results
XX CC in increased yield and stability of Apo-2 ligand trimers
XX SQ Sequence 281 AA;
Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
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RESULT 15
AAE11031
XX ID AAE11031 standard; protein; 281 AA.
XX AC AAE11031;
XX DT 18-DEC-2001 (first entry)
XX

```

Human TNF related apoptosis inducing ligand (TRAIL) protein.

Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
melanoma.

Homo sapiens.

Key Location/Qualifiers
Domain 1..18
Region 19..38
Domain 39..281
Domain /label= Extracellular_domain

US6284236-B1.
04-SEP-2001.
26-MAY-1999; 99US-00320424.
29-JUN-1995; 95US-00496632.
01-NOV-1995; 95US-00548368.
25-JUN-1996; 96US-00670354.
26-MAR-1998; 98US-00048641.
10-NOV-1998; 98US-00190046.
(IMMV) IMMUNEX CORP.
Wiley SR, Goodwin RG;
WPI; 2001-595463/67.
N-PSDB; AAD18395.

New tumor necrosis factor related apoptosis inducing ligand polypeptides
for treating viral infections (e.g. bovine viral diarrhoea or human
immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).

Claim 2; Col 45-48; 41pp; English.

The invention relates to a cytokine designated as tumour necrosis factor
(TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
of certain target cells, including cancer cells and virally infected
cells. The TRAIL polypeptides are useful in killing cancer cells, in
treating viral infections (e.g. bovine viral diarrhoea or human
immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
melanoma), as a research reagent useful in studying apoptosis including
the regulation of programmed cell death. TRAIL DNA sequences may be
employed in developing a gene therapy approach to treating disorders
mediated by defective or insufficient amounts of TRAIL, in the production
of TRAIL polypeptides and as probes or primers in polymerase chain
reactions (PCR). The present sequence is human TRAIL protein

Sequence 281 AA;

Query Match 100.0%; Score 1478; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
Db 1 MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVFTNELKQMDKYSGIACFLKE 60
Qy 61 DDSYWDNDPNDRESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Db 61 DDSYWDNDPNDRESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPLVRERGPO 120
Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVIEHKG 180
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Qy 181 FYIYSQTYFRFQEBIKENTKNDKQVQYIYKYTSYDPDILMKSRNSCWSKDAEYGLY 240
Db 181 FYIYSQTYFRFQEBIKENTKNDKQVQYIYKYTSYDPDILMKSRNSCWSKDAEYGLY 240
Qy 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281
Db 241 SIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

QY 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
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 Db 181 FYYISQTYFRFOBEIKENTKNDKQWQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 240
 |||||
 QY 241 SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
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 Db 241 SIYGGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLVG 281
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=> s human Fas ligand
L1 370 HUMAN FAS LIGAND

=> s l1 and mouse fas ligand
L2 7 L1 AND MOUSE FAS LIGAND

=> dup remove l2
PROCESSING COMPLETED FOR L2
L3 3 DUP REMOVE L2 (4 DUPLICATES REMOVED)

=> d l3 1-3 cbib abs

L3 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
1996:61419 Document No. 124:115474 Use of Fas ligand to suppress T lymphocyte-mediated immune responses. Bellgrau, Donald; Duke, Richard C. (University of Colorado, USA). PCT Int. Appl. WO 9532627 A1 19951207, 50 pp. DESIGNATED STATES: W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ, VN; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1995-US6742 19950526. PRIORITY: US 1994-250478 19940527; US 1995-378507 19950126.

AB Soluble mouse and **human Fas ligand** polypeptides and methods are useful for inhibiting T-lymphocyte-mediated immune responses, treating inflammation or preventing transplant rejection. The Fas ligand may be provided to the recipient mammal by a variety of means, including by direct administration of the Fas ligand or by providing the gene encoding the Fas ligand to a subject such that Fas ligand is synthesized by the subject. Also, antibody and monoclonal antibody against the mouse and **human Fas ligand** epitopes are claimed.

L3 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

1996:402030 Document No. 125:84664 Novel mammalian Fas ligands and cDNAs encoding them and their use in the therapeutic regulation of apoptosis. Nagata, Shigekazu; Suda, Takashi; Takahashi, Tomohiro; Nakamura, Norio (Mochida Pharmaceutical Co., Ltd., Japan; Osaka Bioscience Institute). Eur. Pat. Appl. EP 675200 A1 19951004, 175 pp. DESIGNATED STATES: R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE. (English). CODEN: EPXXDW. APPLICATION: EP 1994-117761 19941110. PRIORITY: JP 1993-305975 19931110; JP 1993-342526 19931213; JP 1994-74344 19940318; JP 1994-180955 19940708; JP 1994-239363 19940907; JP 1994-278378 19941018.

AB Novel polypeptide ligands for the Fas antigen are identified, purified and characterized and cDNAs encoding them are cloned and expressed. These proteins may be manufactured for regulation of apoptosis by expression of the cloned cDNA for therapeutic use or in the preparation of antibodies. These proteins have a cytoplasmic domain, a transmembrane domain and extracellular domain and takes part in apoptosis. CDNAs for these ligands were cloned by panning of an expression library in COS-7 cells. Monoclonal antibodies to the ligand were prepared and shown to inhibit Fas ligand-induced apoptosis. Antisense oligonucleotides to the Fas gene were able to inhibit gene expression.

L3 ANSWER 3 OF 3 MEDLINE on STN DUPLICATE 1
95071350. PubMed ID: 7980502. Role of Fas ligand in apoptosis induced by hepatitis C virus infection. Mita E; Hayashi N; Iio S; Takehara T; Hijioka T; Kasahara A; Fusamoto H; Kamada T. (First Department of Medicine, Osaka University School of Medicine, Japan.) Biochemical and biophysical research communications, (1994 Oct 28) 204 (2) 468-74. Journal code: 0372516. ISSN: 0006-291X. Pub. country: United States. Language: English.

AB To investigate the role that Fas ligand plays in the apoptosis of hepatocytes induced by hepatitis C virus infection, we isolated a cDNA clone for **human Fas ligand** and examined the expression of Fas ligand in liver-infiltrating mononuclear cells obtained from patients with chronic hepatitis C. The amino acid sequence of **human Fas ligand** showed 76% and 77% identity with those of rat and **mouse Fas ligand**, respectively. When the expression of Fas ligand transcripts was tested by reverse transcription-polymerase chain reaction, the amplified signal was detected in liver-infiltrating mononuclear cells and peripheral blood mononuclear cells, whereas only a weak signal or none at all was detected in liver tissues. These findings suggest that the Fas ligand-Fas antigen system may play an important role in liver cell injury by hepatitis C virus infection.

=> s ruben s?/au

L4 1444 RUBEN S?/AU

=> s 14 and "AIM"

L5 21 L4 AND "AIM"

=> dup remove 15

PROCESSING COMPLETED FOR L5

L6 14 DUP REMOVE L5 (7 DUPLICATES REMOVED)

=> d 16 1-14 cbib abs

L6 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

2004:39584 Document No. 140:87695 A new member of the TNF ligand superfamily and its use in treating immune disorders. Ebner, Reinhard; Yu, Guo-Liang; **Ruben, Steven M.**; Zhai, Yifan; Ullrich, Stephen (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2004009147 A1 20040115, 189 pp., Cont.-in-part of U.S. 6,635,743. (English). CODEN: USXXCO. APPLICATION: US 2003-375680 20030228. PRIORITY: US 1996-PV13923 19960322;

US 1996-PV30157 19961031; US 1997-822953 19970321; US 1998-3886 19980107; US 1998-27287 19980220; US 1998-PV75409 19980220; US 1999-252656 19990219; US 1999-PV124041 19990311; US 1999-PV137457 19990604; US 1999-PV142657 19990706; US 1999-PV148326 19990811; US 1999-PV168380 19991202; US 2000-523323 20000310; US 2002-PV360234 20020301.

AB A new member of the human TNF-Ligand superfamily, Apoptosis Inducing Mol. II (**AIM II**) is identified by sequence homol. for use in the treatment of immune disorders. The protein is a ligand for the TNF receptor TR6 and so may be used for the therapeutic induction of apoptosis or as a target for new drugs for the therapeutic inhibition of apoptosis. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 2 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 1

2003:537115 Document No.: PREV200300537649. Apoptosis inducing molecule II and methods of use. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; Ruben, Steven M. [Inventor]; Ullrich, Stephen [Inventor]; Zhai, Yifan [Inventor]. Guilford, CT, USA. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6635743 October 21, 2003. Official Gazette of the United States Patent and Trademark Office Patents, (Oct 21 2003) Vol. 1275, No. 3. <http://www.uspto.gov/web/menu/patdata.html>. e-file.

ISSN: 0098-1133 (ISSN print). Language: English.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid molecules are provided encoding a human Apoptosis Inducing Molecule II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft versus host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 3 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN 2003:70974 Document No.: PREV200300070974. Apoptosis Inducing Molecule II and methods of use. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; Ruben, Steven M. [Inventor]; Zhang, Jun [Inventor]; Ullrich, Stephen [Inventor]; Zhai, Yifan [Inventor]. Rockville, MD, USA. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6495520 December 17, 2002. Official Gazette of the United States Patent and Trademark Office Patents, (Dec 17 2002) Vol. 1265, No. 3. <http://www.uspto.gov/web/menu/patdata.html>. e-file.

ISSN: 0098-1133 (ISSN print). Language: English.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid molecules are provided encoding a human Apoptosis Inducing Molecule II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft versus host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 4 OF 14 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

2003:42575 Document No.: PREV200300042575. Apoptosis inducing molecule II. Ebner, Reinhard [Inventor, Reprint Author]; Yu, Guo-Liang [Inventor]; **Ruben, Steven M.** [Inventor]. ASSIGNEE: Human Genome Sciences, Inc.. Patent Info.: US 6479254 November 12, 2002. Official Gazette of the United States Patent and Trademark Office Patents, (Nov 12 2002) Vol. 1264, No. 2. <http://www.uspto.gov/web/menu/patdata.html>. e-file. ISSN: 0098-1133 (ISSN print). Language: English.

AB The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis Inducing Molecule II (**AIM II**). In particular, isolated nucleic acid molecules are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft versus host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 5 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

2002:488138 Document No. 137:57591 Apoptosis inducing Molecule II and methods of use. Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Zhang, Jun; Ullrich, Stephen; Zhai, Yifan (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2002081647 A1 20020627, 96 pp., Cont.-in-part of U.S. Ser. No. 27,287. (English). CODEN: USXXCO. APPLICATION: US 1999-252656 19990219. PRIORITY: US 1996-PV13923 19960322; US 1996-PV30157 19961031; US 1997-822953 19970321; US 1998-3886 19980107; US 1998-27287 19980220; US 1998-PV75409 19980220.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis Inducing Mol. II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 6 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

2002:409195 Document No. 137:1567 Human apoptosis inducing molecule II and its cDNA and use thereof in drug screening and therapy. Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Ullrich, Stephen (Human Genome Sciences, Inc., USA). U.S. Pat. Appl. Publ. US 2002064869 A1 20020530, 79 pp., Cont.-in-part of U.S. Ser. No. 822,953, abandoned. (English). CODEN: USXXCO. APPLICATION: US 1998-27287 19980220. PRIORITY: US 1996-PV13923 19960322; US 1996-PV30157 19961031; US 1997-822953 19970321.

AB The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis Inducing Mol. II (**AIM II**). In particular, isolated nucleic acid mols. are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The effect of **AIM II** on the cell growth are tested in breast cancer cell line or xenograft human breast carcinoma cell MDA in nude mice. Soluble **AIM II** can mediate cytotoxicity in HT-29 cell and stimulate secretion of IFN γ in human PBL cells. Cell surface expression of β -lymphokine receptor fusion protein LT β R-Fc or TR2-Fc fusion protein can block soluble **AIM II**-mediated cytotoxicity in HT-29 cells and **AIM II** can bind to LT β R specifically. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 7 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
2000:645884 Document No. 133:242574 Apoptosis-inducing molecule II and for antitumor, antiarthritic, antiautoimmune, and other therapeutic use. Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Zhai, Yifan; Ullrich, Stephen (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 2000053223 A1 20000914, 388 pp. DESIGNATED STATES: W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US6332 20000310. PRIORITY: US 1999-PV124041 19990311; US 1999-PV137457 19990604; US 1999-PV142657 19990706; US 1999-PV148326 19990811; US 1999-PV168380 19991202.

AB The present invention relates to a novel member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis Inducing Mol. II (**AIM II**). **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 8 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
2000:628154 Document No. 133:236828 Tumor necrosis factor receptors 6 α and 6 β . Gentz, Reiner L.; Ni, Jian; Ebner, Reinhard; Yu, Guo-liang; **Ruben, Steven M.**; Feng, Ping (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 2000052028 A1 20000908, 332 pp. DESIGNATED STATES: W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US5686 20000303. PRIORITY: US 1999-PV121774 19990304; US 1999-PV124092 19990312; US 1999-PV131279 19990427; US 1999-PV131964 19990430; US 1999-PV146371 19990802; US 1999-PV168235 19991201.

AB The present invention relates to novel Tumor Necrosis Factor Receptor proteins. In particular, isolated nucleic acid mols. are provided encoding the human TNFR-6 α and -6 β proteins. TNFR-6 α and -6 β polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of TNFR-6 α and -6 β activity. Also provided are diagnostic methods for detecting immune system-related disorders and therapeutic methods for treating immune system-related disorders.

L6 ANSWER 9 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
1999:549380 Document No. 131:180813 Apoptosis-inducing molecule II, its encoding cDNA sequence, and therapeutic and clinical uses. Ebner, Reinhard; Yu, Guo-Liang; **Ruben, Steven M.**; Zhang, Jun; Ullrich, Stephen; Zhai, Yifan (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 9942584 A1 19990826, 224 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,

SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US3703 19990219. PRIORITY: US 1998-PV75409 19980220; US 1998-27287 19980220.

AB The present invention relates to a member of the TNF-Ligand superfamily. More specifically, isolated nucleic acid mols. are provided encoding a human Apoptosis-Inducing Mol. II (**AIM II**). The nucleic acid was discovered in a cDNA library derived from human macrophage ox LDL, and shown to contain an open reading frame encoding a protein of 240 amino acid residues. **AIM II** polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. **AIM II** is highly expressed in activated lymphocytes but not in cancer cells. The protein has potent antitumor activity in vivo and in vitro and both lymphotoxin β receptor and TR2 are required for **AIM II**-induced growth inhibition of cancer cells. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, aberrant bone development, autoimmune and other immune system diseases, graft vs. host disease, rheumatoid arthritis, osteoarthritis and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 10 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN

1999:451368 Document No. 131:86868 Cloning and cDNA sequence encoding human apoptosis-inducing molecule II. Ebner, Reinhard; Ruben, Steven M. ; Yu, Guo-liang; Ullrich, Stephen (Human Genome Sciences, Inc., USA). PCT Int. Appl. WO 9935262 A2 19990715, 165 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US242 19990107. PRIORITY: US 1998-3886 19980107; US 1998-27287 19980220.

AB The present invention relates to a member of the tumor necrosis factor ligand superfamily, apoptosis-inducing mol. II (**AIM II**). In particular, isolated nucleic acid mols. are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. **AIM II** is highly expressed in activated lymphocytes but not in cancer cells, and demonstrates enhanced apoptosis and potent in vivo anti-tumor activities. Both lymphotoxin β receptor and TR2 are required for **AIM II**-induced growth inhibition of cancer cells. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 11 OF 14 MEDLINE on STN

DUPLICATE 2

1999123371. PubMed ID: 9924296. Vertical cup/disc ratio in relation to optic disc size: its value in the assessment of the glaucoma suspect. Garway-Heath D F; Ruben S T; Viswanathan A; Hitchings R A. (Glaucoma Unit, Moorfields Eye Hospital, London.) British journal of ophthalmology, (1998 Oct) 82 (10) 1118-24. Journal code: 0421041. ISSN: 0007-1161. Pub. country: ENGLAND: United Kingdom. Language: English.

AB **AIMS:** The vertical cup/disc ratio (CDR) has long been used in the assessment of the glaucoma suspect, though the wide range of CDR values in the normal population limits its use. Cup size is related physiologically to disc size and pathologically to glaucomatous damage. Disc size can be measured at the slit lamp as the vertical disc diameter

2

(DD). The ability of the CDR, in relation to DD, to identify glaucomatous optic discs was investigated. METHODS: 88 normal, 53 early glaucoma, and 59 ocular hypertensive subjects underwent stereoscopic optic disc photography and clinical biometry. Photographs were analysed in a masked fashion by computer assisted planimetry. The relation between vertical cup diameter and DD was explored by linear regression, and expressed in terms of CDR. The upper limit of normal was defined by the 95% prediction intervals of this regression (method 1) and by the upper 97.5 percentile for CDR (method 2). The sensitivity and specificity of CDR to identify an optic disc as glaucomatous was tested with these disc size dependent and disc size independent cut offs in small, medium, and large discs. RESULTS: The CDR was related to DD by the equation $CDR = (-1.31 + (1.194 \times DD))/DD$. The sensitivity in small, medium, and large discs was 80%, 60%, and 38% respectively for method 1 and 33%, 67%, and 63% respectively for method 2. Specificity was 98.9% (method 1) and 97.7% (method 2). CONCLUSIONS: The CDR, relative to disc size, is useful clinically, especially to assist in identifying small glaucomatous discs.

L6 ANSWER 12 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 1997:640681 Document No. 127:288196 Apoptosis-inducing molecule II. Ebner, Reinhard; **Ruben, Steven M.**; Yu, Guo-Liang (Human Genome Sciences, Inc., USA; Ebner, Reinhard; Ruben, Steven M.; Yu, Guo-Liang). PCT Int. Appl. WO 9734911 A1 19970925, 89 pp. DESIGNATED STATES: W: AM, AU, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IL, JP, KG, KP, KR, KZ, LT, LV, MD, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, UA, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1996-US16966 19961031. PRIORITY: US 1996-13923 19960322.

AB The present invention relates to a novel member of the TNF-Ligand superfamily, Apoptosis-Inducing Mol. II (**AIM II**). In particular, isolated nucleic acid mols. are provided encoding the human **AIM II** protein. **AIM II** polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. The invention further relates to screening methods for identifying agonists and antagonists of **AIM II** activity. Also provided are therapeutic methods for treating lymphadenopathy, autoimmune disease, graft vs. host disease, and to inhibit neoplasia, such as tumor cell growth.

L6 ANSWER 13 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
 1997:623179 Document No. 127:315580 Apoptosis-inducing molecule I and its encoding cDNA from human tissues. **Ruben, Steven M.** (Human Genome Sciences, Inc., USA; Ruben, Steven M.). PCT Int. Appl. WO 9733899 A1 19970918, 83 pp. DESIGNATED STATES: W: AM, AU, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KP, KR, KZ, LT, LV, MD, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, UA, US, UZ, VN; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1996-US3773 19960314.

AB The invention relates to apoptosis-inducing mol. I (**AIM-I**) polypeptides, polynucleotides encoding the polypeptides, methods for producing the polypeptides, in particular by expressing the polynucleotides, and agonists and antagonists of the polypeptides. **AIM-I** cDNA was discovered in a cDNA library derived from cells of a human pancreatic tumor and shown to contain an open reading frame encoding 281 amino acid residues with 48.6% similarity and 22.9% identity to human Fas ligand. Northern blot anal. shows that **AIM-I** mRNA is abundant in human heart, bone marrow, CD4+ and CD19+ peripheral blood lymphocytes, and less so in lung and kidney tissue. Cloning of human **AIM-I** cDNA was demonstrated by expression in Escherichia coli using the bacterial expression vector pQE9, expression in a baculovirus expression system using the pA2 vector, expression in COS cells using the pcDNAI/Amp vector, and gene therapeutic expression. The invention further relates to methods for utilizing such polynucleotides, polypeptides,

agonists and antagonists for applications, which relate, in part, to research, diagnostic and clin. arts.

L6 ANSWER 14 OF 14 MEDLINE on STN DUPLICATE 3
95260771. PubMed ID: 7742276. Pattern electroretinogram and peripheral colour contrast thresholds in ocular hypertension and glaucoma: comparison and correlation of results. **Ruben S T**; Arden G B; O'Sullivan F; Hitchings R A. (Electrodiagnostic Department, Moorfields Eye Hospital, London.) British journal of ophthalmology, (1995 Apr) 79 (4) 326-31. Journal code: 0421041. ISSN: 0007-1161. Pub. country: ENGLAND: United Kingdom. Language: English.

AB **AIMS**--Both pattern electroretinogram and peripheral colour contrast thresholds have been shown to be abnormal in glaucoma and ocular hypertension. This study evaluates each of these tests as tools for the early diagnosis of glaucoma, compares and contrasts the results, and examines the relation between the two tests in a large cohort of ocular hypertensive patients. **METHODS**--Transient and steady state pattern electroretinograms and peripheral colour contrast thresholds were performed in 45 normal, 37 glaucomatous, and 206 ocular hypertensive eyes. The results were analysed using receiver operating characteristic curves, together with evaluation of sensitivity and specificity of the tests. The relation between the two tests was examined by direct statistical correlation of the results. **RESULTS**--All tests showed high sensitivity and specificity for discriminating between normal and glaucomatous eyes. However, there was a significant difference between the two tests for the number of ocular hypertensives considered as abnormal. Forty per cent of ocular hypertensives had abnormal pattern electroretinogram compared with 30% with abnormal peripheral colour vision. Peripheral colour contrast thresholds showed a significant correlation with both transient and steady state pattern electroretinogram. **CONCLUSION**--Both of these tests have been shown to be promising new tools for the early detection of glaucoma but the number of ocular hypertensive patients showing abnormal results is rather higher than expected considering the natural history of the condition. Sensitivity in ocular hypertension may be increased by using a combination of both tests. The significant correlation between these psychophysical and electrophysiological tests is discussed.

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---Logging off of STN---

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Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	57.28	57.49
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	-7.62	-7.62

STN INTERNATIONAL LOGOFF AT 14:08:52 ON 23 MAR 2004